/*tag= a /note= "these residues have N3'->P5' phosphoramidate

linkages"

Location/Qualifiers

1..15 /*tag=

Key misc_feature

Synthetic

Oligonucleotide containing phosphoramidate linkages. phosphoramidate linkage; solid phase synthesis; ss.

(first entry)

25-MAR-2003 31-MAR-1998

AAV01604;

BP.

AAV01604 standard; DNA; 15

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A new method is provided for the synthesis of oligonucleotides having (N3'->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected antino nucleoside to a solid support; (b) deprotecting the 3'-amino; (c) reacting with a 3'-protected aminouncleoside-5'-phosphoramidite link; (d) oxidising this link to phosphoramidate; and phosphoramidate link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b)-(d) until the required oligonucleotide of is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large scale. The obtained oligos, containing phosphoramidate linkages, have favourable binding properties, nuclease resistance and solubility, and are useful as research, diagnostic and therapeutic agents. The present sequence is an example of an oligonucleotide in which N3'->PS' (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                    a
These residues have N3'->P5' phosphoramidate
linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidite then oxidation, useful as research, diagnostic and therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirschbein BL, McCurdy SN;
                                                                                                                                    Oligonucleotide containing phosphoramidate linkages.
                                                                                                                                                                   phosphoramidate linkage; solid phase synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 28; 60pp; English.
                             AAV01603 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                            96WO-US10418.
                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0603566.
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                                                                                           (updated)
(first entry)
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gryaznov SM,
Schultz RG;
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/*tag=
/note=
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                                                                                                                                                                                                                              Key
misc_feature
                                                                                                                                                                                                                                                                                                                            WO9731009-A1.
                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1996;
                                                                                        25-MAR-2003
31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                           28-AUG~1997.
                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fearon KL,
Nelson JS,
                                                                                                                                                                                                    Synthetic
                                                            AAV01603;
RESULT 717
                AAV01603/c
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Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidite then oxidation, useful as research, diagnostic

Disclosure; Page 28; 60pp; English.

and therapeutic agents

Gryaznov SM, Hirschbein BL, McCurdy SN; Schultz RG;

WPI; 1997-435080/40.

Fearon KL, Nelson JS,

(LYNX-) LYNX THERAPEUTICS INC.

96US-0603566. 96US-0603566. 96WO-US10418.

14-JUN-1996;

21-FEB-1996; 21-FEB-1996;

WO9731009-A1

28-AUG-1997.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new method is provided for the synthesis of oligonucleotides having a N3'->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected amino nucleoside to a solid support; (b) deprotecting the phosphoramidite manomer to form an internucleoside N3'-> p5' phosphoramidite monomer to form an internucleoside N3'-> p5' phosphoramidite link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b) (d) until the required oligonucleotide is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large favourable binding properties, nuclease resistance and solubility, and are useful as research, diagnostic and therapeutic agents. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is an example of an oligonucleotide in which N3'->P5' phosphoramidate linkages have been introduced by the new method. (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
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100.0%; Pre
0; }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ID AAV074:
XX
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Matches
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Gaps

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1084 AAAAAAAAAAA 1098

à q

15 AAAAAAAAAAAA 1

RESULT 718 AAV01604

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oligonucleotide; peptide; conjugate; release tag compound; mass spectrometry; detection; identification; diagnosis; primer; ss.
                                                                                                                                                                                                      New release tag compounds for detecting target molecule(s) - comprising a reactive group, a release group and a releasable non-volatile mass label detectable by mass spectrometry
                             Synthetic peptide-labeled oligonucleotide primer.
                                                                                                                                                                                                                                     Example 3; Page 92; 170pp; English.
                                                                                                                                                          (GENE-) GENETRACE SYSTEMS INC
                                                                                                                    97WO-US22639.
                                                                                                                                   97US-0046719.
96US-0033037.
                                                                                                                                                                         Montforte JA,
                (first entry)
                                                                                                                                                                                        WPI; 1998-348547/30.
                27-OCT-1998
                                                                                                                   10-DEC-1997;
                                                                                                                                   16-MAY-1997;
10-DEC-1996;
                                                                                    WO9826095-A1
                                                                                                    18-JUN-1998
                                                                                                                                                                         CH,
                                                                      Synthetic,
AAV07431
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Shaler TA;

Pollart DJ,

The sequence is that of an oligonucleotide primer which was produced as part of an oligonucleotide peptide conjugate as an example of a part of an oligonucleotide peptide conjugate as an example of a release tag compound (RTC). These comprise a reactive group, a release tag compound (RTC). These comprise a reactive group, a release tag compound (RTC). These comprisend a specific or a reactive group, a synthetic polymer or biopolymer detectable by mass spectrometry. They can be used for e.g. identification of fine. Sequences, identification of non-coding nucleotide sequences, identification of metals, identification of non-coding nucleotide sequence, detection of metals, identification of metals, interactions within a gene or protein sequence, detection of metals, characterisation of antibody-antigen interactions, enzyme-substrate interactions and characterisation of ligand interactions. Multiplex applications include multiple pathogen diagnostics, multiplene genetic genotyping, clone and gene mapping, and gene expression analysis. The RTCs permit the ready detection of releasable mass labels by mass spectroscopy. The releasable mass labels permit the multiplexing of tens, hundreds and perhaps even thousands of different mass labels that can be used to uniquely identify each desired target.

1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; Live 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other; Local Similarity 100. 16s 15; Conservative Query Match Best Loca Matches

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à

AAT86605 standard; DNA; 15 AAT86605; RESULT 720 AAT86605/c

ВP

Oligonucleotide separated by capillary affinity gel electrophoresis.

(first entry)

04-JUN-1998

process using capillary affinity gel electrophoresis. The invention relates to selective separation of electrophoresis. The invention of relates to selective separation of electrically charged target molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer gel. Receptors for target molecules are covalently bound to the polymer. An electric field of at least 50 volts/cm is applied. The capillary tube is charged with the analytical mixture are bound to the receptors and the remaining components are eluted, optionally whilst splitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the affinity of the target molecules for the receptor is eliminated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for selective separation and/or determination of charged organic compounds, and a second electramination of charged organic compounds, and a second electramination of charged organic compounds, and a second electramination of charged organic compounds. ö than prior art processes, especially in the case of complex biological analytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using such as oligonucleotides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification of antibodies, analysis of antisense compounds or screening for enzyme inhibitors. The process achieves higher resolution and selectivity Gaps Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for target molecules are bound gel electrophoresis; separation; polymer-gel; ; 0 Length 15; Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other; Example D3; Page 25; 41pp; English. Paulus A; 97WO-EP02647. 96CH-0001320 15; Conservative Muscate A, Natt F, (NOVS) NOVARTIS AG. WPI; 1998-041763/04 Local Similarity Capillary afinity samples. The deriverandard methods. polyacrylamide; 24-MAY-1996; WO9745721-A1 23-MAY-1997; 04-DEC-1997. Synthetic. Query Match Matches

0; Indels 1.4%; Score 15; DB 1; Lv 100.0%; Pred. No. 3.5e+02; Live 0; Mismatches 0;

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0;

Gaps

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BP. RESULT 721

Capillary afinity gel electrophoresis; separation; polymer-gel; Oligonucleotide linked to polyacrylamide.

us09904568-1.rng

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This sequence represents an example of an oligonucleotide containing novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The sequence is generated synthetically by using an amine-exchange reaction of phosphoramidites in which a deprotected 3'-amino group of an oligonucleotide chain is exchanged for the amino portion of a 5'-phosphoramidite with a protected 3' amino group. The resulting phosphoramidite internucleotide linkage is oxidised to form a stable
                                                                                                                                         /note= "contains internucleotide N3-P5 phosphoramidate internucleotide linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
"contains internucleotide N3-P5 phosphoramidate
internucleotide linkages"
       Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                               McCurdy SN
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the synthesis of oligo-nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N3-P5 phosphoramidate oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Column 33; 34pp; English.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protected phosphoramidate linkage.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                               96US-0771789.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Gryaznov SM,
Schultz RG;
                                                                                                        1..15
/*tag=
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/*tag=
/note=
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                                                                                Key
misc_difference
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                                                                                                                                                                                                                                                                        20-DEC-1996;
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                                                                                                                                                                                                                                                                                                             20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                   14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                 21-FEB-1996;
                                                                                                                                                                                                 US5859233-A.
                                                                                                                                                                                                                                    12-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                           Fearon KL,
Nelson JS,
                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 72
AAX00788
       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an oligonucleotide receptor molecule covalently bound to a polyacrylamide gel via a linking group. The invention relates to selective separation of electrically charged target molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer of polymer. An electric field of at least 50 volts/cm is applied. The capillary tube is charged with the analytical mixture. In a first capillary tube is charged with the analytical mixture are bound to the capillary tube is charged with the analytical mixture are bound to the receptors and the remaining components are eluted, optionally whilst splitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the affinity of the target molecules for the receptor is eliminated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for such as oligonucleotides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification in thibitors. The process achieves higher resolution and selectivity than prior art processes, especially in the case of complex biological analytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using standard methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                            a
"Thymine at 5' end attached to a polyacrylamide
gel via a linking group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for target molecules are bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example A1; Page 22; 41pp; English.
                                                                                                                                                                                                                                                                                                                                           Paulus A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 AAAAAAAAAAA 1098
                                                                                                                                                                                                                            97WO-EP02647
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                                                                          /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                         Muscate A, Natt F,
                                                                                                                                                                                                                                                                                                   (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-041763/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 15; Conserv
                                   Key
modified_base
                                                                                                                                                 WO9745721-A1
                                                                                                                                                                                                                                                                24-MAY-1996;
                                                                                                                                                                                                                            23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-APR-1999
                                                                                                                                                                                       04-DEC-1997
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX00787;
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AAX00787/C
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AC
AC
AC
AC
DT
13-APR
XX
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Gaps

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The present primer was used to reverse transcribe human RNA, from which a cDNA sequence encoding a protein with heparanase catalytic activity was amplified. The heparanase (hap) polynuclectide is useful in gene therapy, particularly in treating tumour, inflammation or autoimmunity. Particularly, the polynuclectide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g. bFGF) and cytokines (e.g. interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynuclectide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, arthroadclerosis, inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome or Creutfieldt-Jakob disease), and some viral,
                                  New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumour, inflammation, autoimmunity, neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conformationally-locked oligonucleotide, antisense inhibitor, bicyclic sugar nucleoside analogue, gene probe; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                               Disclosure; Page 44; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial or protozoa infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J= e
base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ААААААААААААА 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA62347 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
/mod_bae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
WPI; 2000-579289/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA62347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA62347,
à
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                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an example of an oligonuclectide containing novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The sequence is generated synthetically by using an amine-exchange reaction of phosphoramidites in which a deprotected 3'-amino group of an oligonucleotide chain is exchanged for the amino portion of a 5'-phosphoramidite with a protected 3' amino group. The resulting phosphoramidite internucleotide linkage is oxidised to form a stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heparanase; gene therapy; tumour; inflammation; autoimmunity; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                             New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers used in the synthesis of oligo-nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                      McCurdy SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 15; DB 1; Le:
100.0%; Pred. No. 3.5e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used to reverse transcribe human RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INSI-) INSIGHT STRATECY & MARKETING LTD.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
(FRIE/) FRIEDMAN M M.
                                                                                                                                                                                                    Gryaznov SM, Hirschbein BL,
Schultz RG;
                                                                                                                                                                                                                                                                                                                                                    Example 10; Column 33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feinstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protected phosphoramidate linkage.
                                                                                                                                                            (LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA75048 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 AAAAAAAAAAAA 1098
                                                                               96US-0771789.
96US-0603566.
96US-0663918.
                                              96US-0771789.
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Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                                                                                                                                                         WPI; 1999-120007/10.
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                                                                             20-DEC-1996;
21-FEB-1996;
14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1999;
                                            20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
        12-JAN-1999
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                                                                                                                                                                                                Fearon KL,
Nelson JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pecker I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA75048;
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AAA75048/c
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Gaps

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The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-C.3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3'.5'-bridged nucleosides which can be used as building blocks for oligonucleotides oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
                                                                                                                                                                                                                                                                                                                               New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
    /mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
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/mod_base= OTHER
/note= "3'-C-amino-5'{S}-C,3'-N-ethanothymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAA 1098
                                                                                                                                      99US-0309742.
                                                                                                                                                                          99US-0309742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene-specific diagnostics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AAAAAAAAAAAAA
                                                                                                                                                                                                              (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                           WPI; 2000-451496/39.
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
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                                                                                                                                      11-MAY-1999;
                                                                                                                                                                          11-MAY-1999;
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                                                            US6083482-A
                                                                                                04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                       diagnostics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                      Wang G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
                                                                                                                                                                                                                                                                                                                                                                                                 New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/mcd_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
mod_base= OTHER
'note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                          'note = "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conformationally-locked oligonucleotide, antisense inhibitor, bicyclic sugar nucleoside analogue, gene probe, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4%; Score 15; DB 1; Length 15; 0.0%; Pred. No. 3.5e+02; 0.0% Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 20; Column 15; 10pp; English.
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                                                        *tag= g
mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                              99US-0309742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene-specific diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                       (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-451496/39.
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified base
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                                    modified base
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                                                                                                                                                                                                                                                11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                             Wang
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PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-mannanase enzyme, which is involved in the hydrolysis of polysaccharides that consist of molecules of mannan, either simple or branched, linked together by beta(1-4) bonds. The mannanase polynucleotide sequence is used for in vivo modification of the coffee endo-beta-mannanase gene. It is also used to produce transgenic plant cells (especially coffee cells) which have modified properties of mannan polysaccharide, and thus altered flavour or structure. The enzyme is used for modification, degradation or synthesis of mannan polysaccharide, and thus altered flavour or the increase the percentage of dry matter extraction, and thus reduce the quantity of sediment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  their pharmaceutically moderate salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides modified nucleomonomers of specified formula and
pharmaceutical, cosmetic or food compositions to hydrolyze polymannans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 20; 42pp; English.
                                                              Disclosure; Page 32; 41pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequence of ODN-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psoriasis; duplex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNE-) UNIV NEBRASKA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200011013-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence where incorporated by phosphoramidite chemistry using a DNA synchesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics.
                                                                                                                                                                                                                                                                                   New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer used to amplify DNA encoding an endo-beta-mannanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 15; DB 1; Length 15; 00.0%; Pred. No. 3.5e+02; Ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Example 20; Column 16; 10pp; English
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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                                                                                                        99US-0309742.
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                                                              99US-0309742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROD NESTLE
                                                                                                                                                 (ICNC ) ICN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1999;
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                                                              11-MAY-1999;
                                                                                                        11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                               diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer;
                  04-JUL-2000
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                                                                                                                                                                                             Wang G;
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inflammatory conditions, cardiovascular disorders, immune reactions, cancer, vival infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stablity when hybridizing to target mucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAA07788-803 represent oligomucleotides forming a third strand along with the duplex sequences.
fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as
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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels 1084 AAAAAAAAAAAA 1098

15 AAAAAAAAAAAA 1

AAA07789 standard; DNA; 15 RESULT

ВP

(first entry) 23-JUN-2000 AAA07789;

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss. Nucleic acid sequence of ODN-b.

Synthetic.

WO200011013-A1

02-MAR-2000

99WO-US19029 20-AUG-1999; 98US-0097712 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

their pharmaceutically acceptable salts. The nucleomoners are used monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, The invention provides modified nucleomonomers of specified formula and

factors and interleuking associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for) oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences. growth oncogenes, cytokines, adhesion molecules, receptor molecules,

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;

Gaps ; 0 1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels 15; Conservative Local Similarity Query Match Best Loca Matches

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1084 AAAAAAAAAAAA 1098 AAAAAAAAAAAA 1

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Gaps

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RESULT 731

AAA07790 standard; DNA; 15 BP. AAA07790/c

AAA07790;

(first entry) 23-JUN-2000

Nucleic acid sequence of ODN-c.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; viral infection; infla psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000

99WO-US19029. 20-AUG-1999; 98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

their pharmaceutically modified sails. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic and molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as The invention provides modified nucleomonomers of specified formula and

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inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stablity when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences.
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Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

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Gaps
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0
Score 15; DB 1; Length 15;
Pred. No. 3.5e+02;
                     0; Indels
     100.0%; Pred. no.
  1.48;
                       15; Conservative
  Query Match
Best Local Similarity
                        Matches
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1084 AAAAAAAAAAAA 1098 Н AAAAAAAAAAAA 15 ð a

AAA07791 standard; DNA; 15 AAA07791,

BP.

(first entry) 23-JUN-2000

Nucleic acid sequence of ODN-d

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

99WO-US19029. 20-AUG-1999;

98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA,

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure, Page 20; 42pp; English.

their pharmaceutically accepted matter. The nucleomoners are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for invention provides modified nucleomonomers of specified formula and

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their pharmaceutically acceptable sails. The nucleomnomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA
             Oligomers comprising the nucleononomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target of stable association. Sequences AAAA07788-803 represent oligomucleotides forming a third strand along with the duplex sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention provides modified nucleomonomers of specified formula and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics
for which the oligomers are suitable for).
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                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                       Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;
                                                                                                                                                                                                                          DB 1; Le
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                          Score 15;
Pred. No.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA07792 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                            Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                       1084 AAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis; duplex; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA07792;
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B;
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physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences. stability when hybridizing to target nucleic acid sequences, are 888888888888

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Length 15; 0; Indels 1.4%; Score 15; DB 1; De 100.0%; Pred. No. 3.5e+02; 1000.0%; Prec. ... 0; Mismatches 1084 AAAAAAAAAAAA 1098 Conservative Local Similarity 15; Query Match Matches ð

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Gaps

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AAAAAAAAAAAA 1 15 g

AAA07793 standard; DNA; 15

BP.

Nucleic acid sequence of ODN-f. (first entry) 23-JUN-2000 AAA07793;

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic

WO200011013-A1.

02-MAR-2000

99WO-US19029.

98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics Modified nucleomonomers, u oligomers used to inhibit

Disclosure; Page 20; 42pp; English

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regularion, cancer and virally-infected cells. They are used in oligomers for gene regularion, cancer and virally-infological samples such as those containing pathogenic bacteria, consistences, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth carcors and interleukins associated with pathological conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while AAAO 7793/C

AAAO 7793/C

AAAO 7793/C

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AAAO 799/C

XXX AAAO 7793/C

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XXX B

their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, and carried ampless uch as those containing pathogenic bacteria, in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth a cators and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections dee Analynse for oligomers comprising the nucleomonomers exhibit increased duplex DNA stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target ó, maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO/7788-803 represent oligonucleotides forming a third strand along with the duplex sequences. Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; The invention provides modified nucleomonomers of specified formula and Gaps non-toxic Modified nucleomonomers, used in physiologically stable, non-toxicoligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics 0; Length 15; Indels 3.5e+02; DB 1; Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other; 1.4%; Score 15; DB 100.0%; Pred. No. 3.5 Disclosure; Page 20; 42pp; English Nucleic acid sequence of ODN-g. 1084 AAAAAAAAAAAA 1098 AAA07794 standard; DNA; 15 BP 99WO-US19029. 98US-0097712. AAAAAAAAAAAA 1 (first entry) Query Match Best Local Similarity 100.0 Matches 15; Conservative psoriasis; duplex; ss, (UYNE-) UNIV NEBRASKA WPI; 2000-246530/21. WO200011013-A1. 20-AUG-1999; 22-AUG-1998; 23-JUN-2000 02-MAR-2000 Synthetic. 15 AAA07794; Sold B; AAA07794/ RESULT ద 88888888 à

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nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences.
                                                                                                                      Seguence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
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Query Match
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 1084 AAAAAAAAAAAAA 1098 15 AAAAAAAAAAAA 1 à 셤

Nucleic acid sequence of ODN-h AAA07795 standard; DNA; 15 BP 23-JUN-2000 (first entry) AAA07795;

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000

99WO-US19029. 20-AUG-1999; 98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA.

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

their pharmaceutically acceptable sailes. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutically acceptable sailes. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, dancer and virally infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones, serum proteins, achesion molecules, receptor molecules, cytokines, oncoden RNAs that encode enzymes, hormones, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for).

Coligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into calls while maintaining stringent base pair fidelity for target DNA sequences. The maintaining stringent base pair fidelity for target DNA sequences. The coligomers demonstrate significant single- or coluble-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides invention provides modified nucleomonomers of specified formula and

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                                                                Length 15;
                                                                                                   Indels
forming a third strand along with the duplex sequences.
                              Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
                                                                1.4%; Score 15; DB 1; Le:
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                      Conservative
                                                                               Local Similarity
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Matches
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Gaps

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Gaps

0;

AAA07796/c RESULT 737

AAA07796 standard; DNA; 15 BP AAA07796;

Nucleic acid sequence of ODN-i. 23-JUN-2000

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000.

99WO-US19029. 20-AUG-1999; 98US-0097712 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

non-toxic Modified nucleomonomers, used in physiologically stable, non-toxicoligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

their pharmaceutically acceptable sails. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antiense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO/786 for details of other uses for which the oligomers are suitable for).

Oligomers comprising the nucleomonomers exhibit increased duplex DNA reability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO/788-803 represent oligonucleotides forming a third strand along with the duplex sequences. invention provides modified nucleomonomers of specified formula and

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Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.
                                  Gaps
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                                  0;
               Score 15; DB 1; Length 15;
Pred. No. 3.5e+02;
0; Mismatches 0; Indels
Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;
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                ch 1.4%; Sco
l Similarity 100.0%; P:
15; Conservative 0;
                                                                                                                                                                       Nucleic acid sequence of ODN-j.
                                                                                                                  AAA07797 standard; DNA; 15 BP.
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                                                                                                                                                    (first entry)
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                Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                             Synthetic
                                                                                                                                   AAA07797;
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their pharmaceutically acceptable saits. The nucleomoners are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target agenes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, concogenes, growth factors and interleukins associated with pathological conditions such as stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single—or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO7788-803 represent oligonucleotides forming a third strand along with the duplex sequences. The invention provides modified nucleomonomers of specified formula and inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAD7786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA

Seguence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Length 15;

1.4%; Score 15; DB 1; Le 100.0%; Pred. No. 3.5e+02;

Query Match Best Local Similarity

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-inflored cells. They are used in oligomers for gene regulation, cancer acid molecules infected cells. They are used in oligomers for gene regulation, cancer and virally-inflored calls. They are used in oligomers for genes regulation, cancer and virally-inflored calls. They are used in oligomers and enzymes, to target sequences in biological samples such as those containing pathogenic bacteria, canced RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such a cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for).

Coligomers compressing the nucleomonomers exhibit increased duplex DNA catability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to panetrate into cells while mintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences.
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                                                                                                                                                                                                                                                                                                                                                                                          monomer; cancer; gene regulation; antisense technology; leukemia;
infection; inflammatory response; cellular proliferation;
                                        Gaps
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Score 15; DB 1; Le
Pred. No. 3.5e+02;
0; Mismatches 0;
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Query Match 1.4%; Scc
Best Local Similarity 100.0%; P?
Matches 15; Conservative 0;
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                                                                                                                                                                                                                             AAA07798 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                           23-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis; duplex; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                 Nucleomonomer;
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 Mismatches
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                      1084 AAAAAAAAAAAA 1098
                                           15 AAAAAAAAAAAA 1
 15; Conservative
 Matches
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RESULT 740

AAA07799 standard; DNA; 15 BP AAA07799/0 ID AAA0

AAA07799;

(first entry) 23-JUN-2000

Nucleic acid sequence of ODN-1.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1

02-MAR-2000.

20-AUG-1999;

98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for).

Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences.

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;

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Gaps
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Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Gaps

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RESULT 741 AAA07800/c

AAA07800 standard; DNA; 15 BP

AAA07800;

23-JUN-2000 (first entry)

Nucleic acid sequence of ODN-m.

Nucleomonomer; canoer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000

99WO-US19029. 20-AUG-1999;

98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, cancer and virally-infected cells. They are used in oligomers for gene regulation, cancer and virally-infected cells. They are used in oligomers for gene regulation, but and virally-infected cells sumples such as those containing pathogenic bacteria, genes or encoded RNAs that encode enzymes, normones, serum proteins, denesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for).

Coligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The uncleic acid sequences are highly mon-toxic and able to penetrate into cells while maintaining attingent saying the militant singel- or double-extranded target mucleic acid sequences. The coligomers demonstrate significant single- or double-extranded target mucleic acid sequences. The mucleic acid sequences or other forms. nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences.

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

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1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

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15 AAAAAAAAAAAA 1
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AAA07801 standard; DNA; 15 (first entry) 23-JUN-2000 AAA07801;

BP.

Nucleic acid sequence of ODN-n.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000.

99WO-US19029. 20-AUG-1999;

22-AUG-1998;

98US-0097712,

(UYNE-) UNIV NEBRASKA,

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics -

Disclosure; Page 20; 42pp; English.

cells such as bacterial, fungal, yeast, mammalian, cancer and virallyinfected cells. They are used in oligomers for gene regulation,
antisense technology, diagnostic applications to detect trarget sequences
in biological samples such as those containing pathogenic bacteria,
tungi and viruses, oncogenes, growth hormones and enzymes, to target
genes or encoded RNAs that encode enzymes, hormones, serum proteins,
adhesion molecules, receptor molecules, cytokines, oncogenes, growth
factors and interleukins associated with pathological conditions such as
inflammatory conditions, cardiovascular disorders, immune reactions,
cancer, viral infections and bacterial infections (see AAA07786 for
details of other uses for which the oligomers are sultable for).
Oligomers comprising the nucleomonomers exhibit increased duplex DNA
stability when hybridizing to target nucleic acid sequences, are
physiologically stable, non-toxic and able to penetrate into cells while
maintaining stringent base pair fidelity for target DNA sequences. The
Oligomers demonstrate significant single- or double-stranded target
coligomers demonstrate significant single- or double-stranded target
coligomers demonstrate significant form duplexes, triplexes or other forms
of stable association, Sequences AAA07788-803 represent oligomucleotides
forming a third strand along with the duplex sequences. their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in The invention provides modified nucleomonomers of specified formula and

Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;

Gaps . 0 1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity Matches

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AAA07802 standard; DNA; 15 RESULT 743 AAA07802/

AAA07802;

(first entry) 23-JUN-2000

Nucleic acid sequence of ODN-0.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;

psoriasia; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000.

99WO-US19029. 20-AUG-1999; 98US-0097712. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure, Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, artisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungiand viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target comprises or other forms of stable association. Sequences at triplexes or other forms of stable association. Sequences with the duplex sequences.

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

.**,** Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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Gaps

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15 AAAAAAAAAAAA 1

RESULT 744

us09904568-1.rng

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;

psoriasis; duplex; triplex; ss.

WO200011013-A1.

Synthetic.

99WO-US19029.

20-AUG-1999; 22-AUG-1998;

02-MAR-2000,

(UYNE-) UNIV NEBRASKA.

WPI; 2000-246530/21.

Gold B;

Nucleic acid sequence of a strand of triplex oligomer 14.

23-JUN-2000 (first entry)

AAA07825;

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cells such as pacterial, fungal, yeast, mammalian, cancer and virally infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormomes and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, oscupany proteins, adhesion molecules, receptor molecules, vickines, oncogenes, growth full ammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suituble for).

Coligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target or nucleic acid binding activity to form duplaces, tripressing the nucleomonomes, and able or other forms of the calculations of the collisioners demonstrate significant single- or double-stranded target or nucleic acid binding activity to form duplaces, triplered target or the calculations of the calculations of the calculations.
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                                                                                                                                                                                          Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
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                                                                                                                                                     Nucleic acid sequence of ODN-p.
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                       AAA07803 standard; DNA; 15
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                    Synthetic.
                                                              AAA07803;
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invention provides modified nucleomonomers of specified formula and

Disclosure; Page 30; 42pp; English.

non-toxic

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

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their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, artisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target to phological samples such as those containing pathogenic bacteria, adhesion molecules, receptor molecules, cortokines, oncogenes, growth hormones, asrum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth cfactors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for).

Coligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while colligomers demonstrate significant single- or double-stranded target conditions and blading activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO7820-834 represent sequences forming
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Pred. No. 3.5e+02;
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100.0%; Pred. No. co...
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Gaps

0;

AAA07828 standard; DNA; 15 BP.

AAA07828;

AAA07825 standard; DNA; 15 BP.

RESULT 745 AAA07825/c

15

В δ

EXX B

Length 15; 0; Indels

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Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; triplex; ss.
                                                                                                                                                                                                     Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics -
                        Nucleic acid sequence of a strand of triplex oligomer 15.
                                                                                                                                                                                                                                       Disclosure; Page 30; 42pp; English
                                                                                                                                                       (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                      WPI; 2000-246530/21
                                      Nucleomonomer; ca
viral infection;
                                                                                       WO200011013-A1.
                                                                                                                                       22-AUG-1998;
                                                                                                                       20-AUG-1999;
       23-JUN-2000
                                                                                                       02-MAR-2000.
                                                                       Synthetic.
                                                                                                                                                                       3old B;
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Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleid caid sequences, are tability when hybridizing to target nucleid caid sequences. An experimental parable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO7820-834 represent sequences forming cells such as bacterial, fungal, yeast, mammalian, cancer and virallyinfected cells. They are used in oligomers for gene regulation,
antisense technology, diagnostic applications to detect target sequences
in biological samples such as those containing pathogenic bacteria,
fungi and viruses, oncogenes, growth hormones and enzymes, to target
genes or encoded RNAs that encode enzymes, hormones, serum proteins,
adhesion molecules, receptor molecules, cytokines, oncogenes, growth
factors and interleukins associated with pathological conditions such as
inflammanchy conditions, cardiovascular disorders, immune reactions,
cancer, viral infections and bacterial infections (see AAAA07786 for
details of other uses for which the oligomers are suitable for). The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomoners are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in

Gaps .; 1.4%; Score 15; DB 1; Length 15; 00.0%; Pred. No. 3.5e+02; ve. 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other; Query Match 1.4%; Scc Best Local Similarity 100.0%; Pr Matches 15; Conservative 0;

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AAA07831/c ID AAA07831 standard; DNA; 15 AAA07831; RESULT 747 加坡克兹亞

23-JUN-2000 (first entry)

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; Nucleic acid sequence of a strand of triplex oligomer 16.

psoriasis; duplex; triplex; ss.

WO200011013-A1

Synthetic.

02-MAR-2000

99WO-US19029. 20-AUG-1999; 98US-0097712. 22-AUG-1998;

99WO-US19029 98US-0097712.

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics

Disclosure; Page 30; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virallycinfected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and erzymes, to target genes or encoded RNBs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for).

Coligomers comprising the nucleomoners are suitable for) coligomers cancer, when hybridizing to target nucleic acid sequences, the the oligomers acid sequences. The coligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO7820-834 represent sequences forming triplex oligomers

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;

Gaps . 0 Length 15; Indels 1.4%; Score 15; DB 1; Let 0.00.0%; Pred. No. 3.5e+02; ve 0; Mismatches 0; 100.08; Pic Local Similarity 100. Les 15; Conservative Query Match Best Loca Matches

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AAA07834/

AAA07834 standard; DNA; 15 BP

AAA07834;

23-JUN-2000 (first entry) XXXXXXX

Nucleic acid sequence of a strand of triplex oligomer 17.

cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable sales. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleuking associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleit caid sequences, are tability when hybridizing to target nucleit caid sequences. As an anitaining stringent base pair fidelity for target DNA sequences. The nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAAO7820-834 represent sequences forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
                     Nucleomonomer, cancer, gene regulation, antisense technology, leukemia, viral infection, inflammatory response, cellular proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
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Best Local Similarity 100.0%; Pred. No. 3.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30; 42pp; English.
                                                             psoriasis; duplex; triplex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ61854 standard; RNA; 15 BP.
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                                                                                                                                                                                                                                                                 98US-0097712.
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                                                                                                                                            WO200011013-A1
                                                                                                                                                                                                                           20-AUG-1999;
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                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                              Gold B;
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cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and cneained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, and see used to combination with interferon to treat HCV infection, other infectious diseases, autoimmune diseases, and
                                                                                                                                                                                                                                                                                                                 treatment of diseases and conditions related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                          Roberts E,
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100.0%; Pre
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                                                                                                                             99WO-US09027.
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                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC
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                                                                                                                                                                                                                                                                                                               Novel ribozymes for the hepatitis C infection -
                                                                                                                                                                                                                                                          Blatt L, McSwiggen JA,
               autoimmune disease; ss.
                                                                                                                                                                                                                                                                                      WPI; 2000-062023/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                          Hepatitis C virus.
                                                                                                                                                       27-APR-1998;
18-SEP-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2000
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                                                                                                                              26-APR-1999;
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                                                                       WO9955847-A2
                                                                                                                                                                                                    23-MAR-1999;
                                                                                                04-NOV-1999.
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Matches
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WPI; 2001-342909/36.
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modified_base
                                                                                                                                                                                                                           30-OCT-1987;
16-NOV-1990;
                                                                                                                                                                                    04-AUG-1998;
                                                                                                                                                                                                                                                                   12-NOV-1993;
                                                                                                                                             31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                   Dervan PB,
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                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line.

The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepaticillar carcinoma. The ribozymes may be used in combination with interferent to treat HCV infection, other infectious diseases, autoimmune diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·;
                                                                                                                                                                                                                                                                                     Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection \,
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/mod_base= OTHER
/note= "Optionally thymidine has EDTA covalently
attached at C-5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
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                                                                                                                                                                                                       Macejak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.4%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                       Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
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                                                                                                                                                                                                     Blatt L, McSwiggen JA, Roberts E,
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                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 102; 123pp; English.
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                                                                             98US-0100842.
99US-0257608.
99US-0274553.
                                                         98US-0083217.
                   99WO-US09027
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                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
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modified_base
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                   26-APR-1999;
                                                                             18-SEP-1998;
25-FEB-1999;
                                                                                                                      23-MAR-1999;
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This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal naulayisis, and for the isolation and mapping of genes. The present sequence represents probe of the invention used in an example illustrating how the probe binds to and cleaves double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-linked vinyl acetate copolymer carrier material, AIDS treatment, phosphorothioate; solid phase synthesis; modified oligonucleotide; clinical diagnostic; cancer treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide b) for solid phase synthesis of oligonucleotides.
                               /note= "Optionally thymidine has EDTA covalently
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/note= "Phosphorothioate deoxynucleotides"
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
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                                                                   attached at C-5"
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base= OTHER
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90US-0614205.
93US-0152250.
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Best Local Similarity 10v...
These 15; Conservative
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us09904568-1.rng

99US-0140345.

21-JUN-1999;

21-JUN-2000; 2000WO-AU00693.

28-DEC-2000

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This invention describes a novel chemical product comprising a partially hydrolysed cross-linked vinyl acetate copolymer carrier material loaded with nucleotide derivative(s). The product is an intermediate for the large (gram) scale solid phase synthesis of modified oligonucleotides useful e.g. as clinical diagnostics and therapeutics, e.g. for the treatment of AIDS and cancers. The presence of the partially hydrolysed copolymer facilitates the synthesis of larger amounts of oligonucleotides copolymer facilitates the synthesis of larger amounts of oligonucleotides compared with the use of Merckogel (RTM; macroporous polyvinyl acetate) described in Nucleic Acid Res. Sympos Ser. 31, p. 153, 1994.

Compared with the use of Merckogel (RTM; macroporous polyvinyl acetate) described in Nucleic Acid Res. Sympos Ser. 31, p. 153, 1994.

Compared with the use of described in very good quality and high yields, Also, the nucleosides do not display the reduced activity seen in some prior art procedures, less carrier material, reagents and solvent are required. Further, the carrier material, reagents and chus does not present disposal problems. It also swells uniformly in a range of solvents, which contraction during use or solvent exchange.

Compared AMIZOSIO-AMHZOSI3 represent oligonucleotides containing modified
                                                                                                                                                                                                                                                                                                                                  Intermediate for oligonucleotide synthesis comprises partially hydrolysed cross-linked vinyl acetate copolymer loaded with nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 5; 8pp; German.
                                                                                          2000DE-1051726.
                                                                                                                                          99DE-1052376.
                                                                                                                                                                                       (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                     Seliger H, Sobkowski M,
                                                                                                                                                                                                                                                                                       WPI; 2001-336414/36.
DE10051726-A1
                                                                                          18-OCT-2000;
                                                                                                                                          30-OCT-1999;
                                             10-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                       derivative
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Gaps .; 0 Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other; à

1084 AAAAAAAAAAAAA 1098 15 pananananana g

AAF53331 standard; DNA; 15 BP. 30-MAR-2001 (first entry) AAF53331; RESULT 753 AAF53331,

IGF-I oligonucleotide #4291.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytoscatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pityriasis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; the retina; ss.

WO200078341-A1 Homo sapiens

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor IGF9]-1 receptor, IGF binding protein [IGF8P]-2 or IGF8P3), which is capable of infilammation or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scieroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia. Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell Gaps 0; Length 15; 1.4%; Score 15; DB 1; Length 15; 00.0%; Pred. No. 3.5e+02; ve. 0; Mismatches 0; Indels Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other; Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST. Example 8; Page 88; 201pp; English. proliferation and/or inflammation 1.5. 100.0%; Fi 15; Conservative Werther GA, WPI; 2001-041421/05. Best Local Similarity Wraight CJ, Query Match Matches

320 CTGCAGAGAAGCTGT 334 ₽

crecaeaeaacrer 1

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AAF53332 standard; DNA; 15

RESULT 754

AAF53332/ ID AAF5

(first entry)

30-MAR-2001

AAF53332;

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Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disporder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoosis; neophasia; ecleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neobascular condition; hyperplasia; kidney disease; IGF-I oligonucleotide #4292. Homo sapiens.

WO200078341-A1. 28-DEC-2000.

21-JUN-2000; 2000WO-AU00693

99US-0140345.

21-JUN-1999;

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an anticonse oligonuclectide, (for Insulin-like Growth Factor [GGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectide which can be useful for ameliorating the effects of APAF1513-F45161. The method is useful for ameliorating the effects of sociasis, ichthyosis, pityriasis, ruba, pilaris, serbornhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the cetin, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating gastric acid disturbance by administering an oligonucleotide
                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disturbance, gastric reflux, gastritis, dyspepsia, r, duodenal ulcer, Helicobacter pylori, antisense;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 other;
                                                                 Edmondson SR;
                                                                                                                                                                                                                   Example 8; Page 88; 201pp; English.
                               (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF16603 standard; DNA, 15 BP
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                                                               Werther GA,
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Best Local Similarity
Matches 15; Conserv
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stomach ulcer; duod
DNA-RNA hybrid; ss.
                                                                                               WPI; 2001-041421/05
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                                                                 Wraight
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The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori.
which modulates the activity of a polypeptide involved in gastric acid
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of the oligonucleotide (ODN) component of an ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the invention. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties because detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or mismatch discrimination, target or signal amplification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. single-nucleotide mismatch discrimination
                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                        1.4%; Score 15; DB 1; L4 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonuclectide portion of ODN-MGB-LF conjugate.
                                                                                                                                                                                                                                                        Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 other;
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                                                   Example 3; Page 148; 164pp; English
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                   production or secretion -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-328656/34.
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Best Local Similarity
Matches 15; Conserv
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AAF30882/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel polyamide-oligonucleotide derivatives (I) and their physiologically acceptable salts of formula (F(DNA)-Li)_q(PNA-Li)_T(DNA-Li)_g(PNA)_Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-Li)_g(PNA-
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                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyamide-oligonucleotide derivative, anticancer, antiproliferative, antiviral; hepatotropic; vasotropic; antisense inhibition; ribosyme; integrin; cell-cell adhesion; cancer; restenosis; stability; PNA; peptide mulleic acid; ss.
array-based assays and sequencing, including detection of double-stranded DNA by triplex formation. Many different targets can be detected a single reaction vessel. The present DNN-MGB-LF conjugate was used to demonstrate hybridisation-triggered fluorescence. Upon hybridisation to the complementary target sequence there was an increase in fluorescence yield, measured as the ratio of the fluorescence emitted by the hybrid between the ODN-MGB-LF conjugate and its target sequence to the fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                           1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Seguence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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|mod_base= OTHER
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/note= "t-hex"
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95EP-0103332.
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                                                                                                                                                                                                                                                             Local Similarity 100.
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH49243;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 757
                                                                                                                                                                                                                                                                                Matches
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covatent linkage between LNA and PNA, it.e. a bond of a restue containing at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure containing at least one nucleobase different from thymine; and structure containing at least one nucleobase different from thymine; and crowdent bond. The products of the invention have anticancer, antiproliferative, antiviral, hepatotropic and vasotropic activity and can be used for the inhibition of gene expression by antisense, ribozyme, sense, or triple-helix methods, or by binding to proteins (aptamers). (1) are used for treating diseases caused by viruses (human immune deficiency, herpes simplex, influenza, vesicular stomatitis, hepatitis bor papilloma), or mediated by integrins or cell-cell adhesion reactions, for treating cancer, or for inhibiting restenosis, particularly as antisense reagents. They are solvinted in heterogeneous or homogeneous assays, as primers or probes, particularly where the target is amplified before being detected by the integrins or cell-cell adhesion reactions, for complementary strands and better stability in setting the increased affinity for complementary strands and better stability in setting the increased affinity for complementary strands and better stability in serum, associated with conventional peptide nucleic acids (PNA), but lack the disadvantages, i.e. have improved cellular better stability in materials, reduced cytotoxicity, better sequence specificity. They are more active than either DNA or PNA or PNA segments, allowing better discrimination between the pathogenic conditions such as the transition from the properties and non-pathogenic conditions such as the transition from proto-oncogene to oncogene, also, when used as primers, with the PNA component allows additional reactions not possible with the pNA allowing this enzyme to be used to eliminate the engages. Segment of such the PNA allowing this enzyme to be used to eliminate the he
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covalent linkage between DNA and PNA, i.e. a bond or a residue containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
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sc. 100.0%; Fred. No. 3.28
Best Local Similarity 100.0%; Pred. No. 3.29
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99US-0274553. 99US-0274553.

23-MAR-1999; 23-MAR-1999; BLATT L. MCSWIGGEN J A. ROBERTS B.

(BLAT/) | (MCSW/) | (ROBE/) |

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New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme.

Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV inflection in conjunction with one or more other drug therapies,
                                                                                                                                                                                   Roberts B,
8 16:51:41 2004
                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 21; 80pp; English
                                                                                                                                                                                   McSwiggen JA,
                                                                                                                                                                                                                         WPI; 2002-617759/66
                                                                                                                                      MACEJACK D
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                                                                                                                  (PAVC/) (MACE/) I
  Thu Jan
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Macejack D;

Pavco PA,

Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

seqdata.uspto.gov/psipsDIDEntry.html.

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406/c ABX03406 standard; RNA; 15 BP. ABX03406; RESULT 759 ABX03406/(
11D ABX02
AC ABX02
XX ABX02
XX ABX02
XX ABX02
XX Hepat
XX Interview The Structure of Structure of

(first entry) 24-DEC-2002

Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.

Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication; cirrhosis, virucide, liver failure, hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.

Hepatitis C virus.

US2002082225-A1.

27-JUN-2002.

99US-0274553 23-MAR-1999; 99US-0274553 BLATT L. (BLAT/)

23-MAR-1999;

MCSWIGGEN J A. ROBERTS B. PAVCO P A.

(MCSW/) (ROBE/) (PAVC/)

The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme.

Construction The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme.

Construction The present did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma Macejack Pavco PA, Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other; at seqdata.uspto.gov/psipsDIDEntry.html Roberts B, Claim 1; Page 64; 80pp; English. McSwiggen JA, WPI; 2002-617759/66. (MACE/) MACEJACK D. Blatt L,

1.4%; Score 15; DB 1; Le Similarity 100.0%; Pred. No. 3.5e+02; Conservative 0; Mismatches 0; 1084 AAAAAAAAAAAA 1098 Query Match Best Local Simi Matches 15; à

15 AAAAAAAAAAA 1

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0,

Gaps

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Length 15; 0; Indels

> ABQ82140 standard; DNA; 15 ABQ82140; RESULT 760 ABQ82140

11-DEC-2002 (first entry)

Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.

Synthetic.

WO200259294-A1.

01-AUG-2002.

24-JAN-2002; 2002WO-AU00073

26-JAN-2001; 2001US-264067P. 29-NOV-2001; 2001US-333743P.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Helliwell C; Wesley S,

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct,

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WPI; 2002-674959/72
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                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                        The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia col; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation region functional in the eukaryotic cell. The first of reaching with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing large amounts of double-stranded RNA which can be used to convert a DNA fragment into an inverted repeat structure. Plants

C convert DNA fragment into an inverted repeat structure. Plants

C convert by breeding scheme to produce more plants with the same conventional breeding scheme to produce more plants with the same converteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents
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useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer; mutant; tag; tumour suppressor gene; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                           BP; 15 A; 0 C; 0 G; 0 U; 0 other;
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/product= "tag peptide"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                    Claim 14; Page 74; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL49453 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 15; Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutation detection;
protein production;
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                                                                                                                                                                                                                                                                                                                                                           Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL49453;
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Matches
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                                                        Detecting mutations in nucleic acid, useful for diagnosis and characterization of tumors, by amplification, in vitro transcription and translation, then protein detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutation detection; primer; mutant; tag; tumour suppressor gene; protein production; cancer; ds.
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Local Similarity 100.0%; Pred. No. 3.5e+02;
hes 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                             Claim 11; Fig 5; 62pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in the invention.
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P-PSDB; AAO19056.
P-PSDB; AAO19054.
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Detecting mutations in nucleic acid, useful for diagnosis and characterization of tumors, by amplification, in vitro transcription and translation, then protein detection

Claim 11; Fig 5; 62pp; German.

The present invention relates to a method of detecting mutations in a nucleic acid by amplifying the nucleic acid to produce a double-stranded amplicon, in vitro transcription and translation of this amplifor, and detection of the translated protein. The primers used for amplification are designed to produce an amplicon that is translatable and allows differentiation between translation broducts of wild-type and mutated suppressor genes, for (early) diagnosis, monitoring and characterisation of tumours (especially of bladder and intestines) and in the germ line (using nucleic acids from embryos or blood cells). A new multi-tag vector is used to detect or verify the reading frame of a nucleic acid cloned in and to determine the suitability of detectable peptides for analysis and/or purification of a recombinant protein, expressed from a sequence in the vector. The present sequence encodes a tag peptide and was used in the invention. cloned

Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

1.4%; Score 15; DB 1; Length 15; 1.4., 100.0%; Pre-Query Match
Best Local Similarity 100.
Matches 15, Conservative

à 셤 RESULT 763

ABK98141/c

ABK98141 standard; DNA; 15

ABK98141;

(first entry) 07-OCT-2002

Triple helix forming associated oligonucleotide #26.

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic

US6403302-B1,

11-JUN-2002

16-DEC-1993;

17-SEP-1992;

93US-0168920.

(CALY) CALIFORNIA INST OF TECHNOLOGY.

Beal PA; Dervan PB,

WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression -

Example 1; Fig 3B; 108pp; English.

The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid

comprising first and second substantially complementary strands, and an oligonuclectide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonuclectide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression for requiatory sequences of a target gene. The oligonuclectides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific originally bind to pathogenic double-stranded DNA including specific sequence can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonuclectides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonuclectides are capable of forming triple-helices with such sequences in cancerous cells containing the calling or engressing the methods of the present expresents an oligonuclectide cancer invention.

Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

., Length 15; Indels . Score 15; DB 1; Lo Pred. No. 3.5e+02; Query Match Matches Best

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Gaps

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ABK98184

ABK98184 standard; DNA; 15 ABK98184;

BP.

(first entry) 07-0CT-2002

Triple helix forming associated oligonucleotide #48.

formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss. Triple-helix

Synthetic.

US6403302-B1.

11-JUN-2002.

93US-0168920. 16-DEC-1993;

92US-0946976 17-SEP-1992; (CALY) CALIFORNIA INST OF TECHNOLOGY.

Beal PA; Dervan PB,

WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression

Example 7; Fig 24A; 108pp; English

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Raddatz S,
Havens JR,
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     The present invention relates to mentions and origonoriestication forming a triple-helix computating a double helical nucleic acid computating first and second substantially complementary strands, and an oligonuclectide bound to a purine-rich trarget sequence within the double helical nucleic acid, where the oligonuclectide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression is controlled by selective triple-helix formation within expression is regulatory sequences of arget gene. The oligonuclectical and the presence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be selected to specific appropriate pathogenic bacteria or viruses for replication or virulence, reducing their pathogenic bacteria or viruses for replication or virulence, reducing their pathogenic bacteria or viruses for replication or virulence, reducing their pathogenic bacteria or viruses for replication or virulence, reducing their pathogenic bacteria or viruses for replication or virulence, reducing their pathogenic bacteria or viruses for replication or virule oligonuclectides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonuclectides are capable of forming triple-helices with such sequences in cancerous cells containing the cancer causing cell. The present sequence repressing the cancer causing cell. The present sequence represents an oligonuclectide
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present invention relates to methods and oligonucleotides for
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phosphanyloxy)-N'-tritylhexanohydrazide"
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/note= "phosphoramidite linkage"
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Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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'mod_base= "OTHER"
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Best Local Similarity 100.0
Matches 15; Conservative
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Havens JR,
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Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                       The present sequence is of a trityl deprotected hydrazide phosphoramidite 15-mer, designated oligo 09, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and blosensor
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/note= "6-((2Cyanoethoxy)(diisopropylamino)
phosphanyloxy)-N'-tritylhexanohydrazide"
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
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/*tag= b
/note= "phosphoramidite linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macromolecule, hydrazide; immobilisation; ss.
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                                                                                                                                                                                       Example 2; Page 40; 120pp; English
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/mod_base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
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WPI; 2002-401666/43.
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modified_base
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Raddatz S,
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  Havens
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                          Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Windhab N;
                                                                                                                                                                                                                                                           Gaps
                                                                                 The present sequence is of a trityl deprotected hydrazide phosphoramidite 15-mer, designated oligo 031, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface blinding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "4-((2-cyanoethyl)(diisopropylamino)
phosphanyloxymethyl)-benzoic acid methyl
                                                                                                                                                                                                                                                           .;
0
                                     targets, contains phosphorous containing reactive group, hydra
protecting group and benzene ring, and has predefined formula
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                                                                                                                                                                                                                                     1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Hydrazide precursor phosphoramidite oligonucleotide 033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= b
'note= "phosphoramidite linkage"
                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Macromolecule; hydrazide; immobilisation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cy3 dye
                                                                  Example 2; Page 40; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '*tag= a
'mod_base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "OTHER"
                                                                                                                                                                                                                                                                                                                                                 ABL57059 standard; DNA; 15 BP.
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/mod_base= '
/note= "3' (
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                               15 AAAAAAAAAAAA
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         WPI; 2002-401666/43.
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                                                                                                                                                                                                                                                Local Similarity
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                            Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
   phosphanyloxy)methyl)isophthalate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                 phosphoramidite 15-mer, designated oligo 033, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-wand peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding molecies, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
                                                                                                                                                                                                                                                                                sequence is of a hydrazine treated hydrazide precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                         targets, contains phosphorous containing reactive group, hydra
protecting group and benzene ring, and has predefined formula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrazide precursor phosphoramidite oligonucleotide O34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= b
note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mueller-Ibeler J, Schweitzer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macromolecule; hydrazide; immobilisation;
  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag≈ c
/mod_base= "OTHER"
/note= "3′ Cy3 dye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                        Example 3; Page 43; 120pp; English.
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/mod base= "OTHER"
  Greef CH,
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ID ABL57060 standard; DNA; 15
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Onofrey TJ,
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                                                    WPI; 2002-401666/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200214558-A2
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modified_base
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Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula -
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/note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
benzyloxy)-5-((2'-cyanoethyl)(diisopropylamino)
phosphanyloxymethyl)-benzene"
             Windhab N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated oligo 037, which was produced in process from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially MNA, macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
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             Bruecher C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
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Local Similarity 100.0%; Pred. No. 3.5e+02;
hes 15; Conservative 0; Mismatches 0;
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/*tag= b
/note= "phosphoramidite linkage"
           er J, Schweitzer M,
Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macromolecule; hydrazide; immobilisation; ss.
                                                                                                                                                                              Example 3; Page 43; 120pp; English.
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/mod_base= "OTHER"
/note= "3' Cy3 dye"
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         Mueller-Ibeler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAA 1098
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                           Onofrey TJ,
                                                                 WPI; 2002-401666/43
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         Raddatz S,
Havens JR,
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                                                                       Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated oligo 034, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DMA, RNA, peptide mucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hydratidisation based assays, DNA chip technology and biosensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
phenylcarbonylamido)-2-((2''-cyanoethyloxy)
(diisopropyl)amino)-phosphanyloxy)-propane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrazide precursor phosphoramidite oligonucleotide 037.
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/*tag= b
/note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macromolecule; hydrazide; immobilisation; ss.
     Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/mod·base= "OTHER"
/note= "3' Cy3 dye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/mod_base= "OTHER"
--Ris-(3
                                                                                                                                                Example 3; Page 43; 120pp; English
   Greef CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AAAAAAAAAAAA 1
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Best Local Similarity 100.
Matches 15; Conservative
   IJ,
                                     WPI; 2002-401666/43.
Onofrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NANO-) NANOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200214558-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                 applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL57061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 769
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targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula -
                                 Windhab N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Windhab N;
                                                                                                                                                                                   The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated oligo 035, which was produced in an example from the invention and which includes a synthetic branching amidite compound. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
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                                  Bruecher C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schweitzer M, Bruecher C,
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 1; Le
Pred. No. 3.5e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Amino-C6 modification"
                                 Schweitzer M,
CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immobilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "3' Cy3 dye"
                                                                                                                                                              Example 4; Page 44; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
mod_base= "OTHER"
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/mod_base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
                               Mueller-Ibeler J,
Onofrey TJ, Greef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raddatz S, Mueller-Ibeler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-2000; 2000WO-US22205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL57066 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macromolecule; hydrazide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
   (NANO-) NANOGEN INC.
                                                                          WPI; 2002-401666/43
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modified_base
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                               Raddatz S,
Havens JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL57066;
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0
                                                                                Compound for binding macromolecule to substrate surface or conjugation
                Windhab N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
phosphanyloxy)methyl)isophthalate, synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                   The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated cligo 039, which was produced in process for immobilisation of marcomolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of cligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation to surface binding moieties, or for other conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
                                                                                                targets, contains phosphorous containing reactive group, hydrazide
protecting group and benzene ring, and has predefined formula
                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                Bruecher C,
                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrazide precursor phosphoramidite oligonucleotide 035.
                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 1; Le:
Pred. No. 3.5e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
            Mueller-Ibeler J, Schweitzer M,
Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macromolecule; hydrazide; immobilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   branching amidite'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cy3 dye"
                                                                                                                                         Example 3; Page 43; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/mod_base= "OTHER"
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/note= "3' Cy3 dye"
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.4%; SCC
Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                 applications.
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            Raddatz S,
Havens JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL57064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 771
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Gaps

us09904568-1.rng

peptide of the nucleic acid can be used to express membrane-associated or

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Wang

H,

Greef

TŪ,

Onofrey

Havens JR,

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WPI; 2002-401666/43
                                                                    Goldshmidt O,
                             Query Match
                              Best Loca
Matches
                                         ABL40743/
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targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                        in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, propriogy-RNA, proprides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in muleic acid hybridisation based assays, DNA chip technology and biosensor
                                                                                                                                                                                 The present sequence is of an amino-C6-modified and Cy3 dye labeled T15 oligonucleotide that was used in a comparison of hydrazine and amine attachment moieties on active ester surfaces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Le 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 15; DB 100.0%; Pred. No. 3.5
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                                                                                                                             Example 12; Page 57; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL40743 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002034810-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 applications.
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The invention relates to an isolated avian and reptile nucleic acid, encoding a polypeptide with heparanase catalytic activity. The signal

Disclosure; Page 13; 39pp; English.

recombinant proteins

Nucleic acid encoding avian and reptile heparanase polypeptide is useful to treat various heparin-related disorders and the signal peptide is useful in production of membrane-targeted or secreted

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Zcharia

Vlodavsky I, Michal I,

Pecker I,

WPI; 2002-338926/37.

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This invention relates to oligonuclectide analogues comprising a protein nucleic acid molecule (PNA) monomer. They are used in the detection and separation of nucleic acid molecules and as probes, primers, linkers, adapters and antisense agents on solid supports. Modifications enhance their use as capture and detection probes e.g. by the incorporation of biotin, digoxiganen, radioisotopes, fluorescent labels such as fluorescein and reporter molecules such as alkaline phosphatase. They are also used for enhancing or inhibiting the activity of an enzyme or cellular activity. The compounds are stable to nucleases and proteases, have high affinity, binding specificity and solubility. The polyamide backbone of PNAs is resistant to both nucleases and proteases. PNAs bind nucleic acid molecules with greater affinity than DNA or RNA concentration. The compounds are relatively simple to synthesize and care used in a wide variety of applications. This sequence represents a DNA oligomer which is used to represent the effect of single base mismatches on oligonucleotides.
                                                                                                                                                                                                                                                                  ô
        secreted proteins in heterologus expression systems. The encoded polypeptides can be used to prevent tumour angiogenesis, metastasis and invasion, and to intervene with pathologies associated with impaired heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protezoa and bacterial infections or disintegration of neurodegenerative plaques. The present sequence represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotides analogues useful in detection, separation and purification of nucleic acid molecules, comprise monomers, dimers and
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of oligomer # 10 used to compare mismatches.
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0
                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                  0; Indels
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M, Hondorp
                                                                                                                                                                                                                           1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                        Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein nucleic acid molecule; PNA; ds.
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Chakhmakhcheau O, Buryakova A,
                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                        1084 AAAAAAAAAAAA 1098
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30-NOV-2000; 2000US-250334P.
                                                                                                                                                                                                                                                                                                                                                                                                                                7403/c
ABA97403 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                               15 AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                             Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA97403;
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 774
                                                                                                                                                                                                                                                                    Matches
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Thu Jan

AAD22531 standard; RNA; 15 BP.

AAD22531

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Gaps

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The present invention relates to new human pre-adipose cell lines capable to differentiate to white adipose cells, exhibiting essentially the same cellular properties of normal white adipose cells. The human pre-adipose cell lines are useful for the identification of substances controlling the regulation of lipid uptake and release by human white adipocytes, and substances controlling the differentiation of preadipocytes into mature adipocytes. They are useful for screening compounds capable to regulate the secretion of any metabolites or hormones from human white adipocytes. Sequences of the invention are useful for developing drugs, food ingredients and supplements against obesity, diabetes and cardio-
                                                                                                                                                                                                                                                                                                                                                                                                                        Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid; diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular diseases. The present DNA sequence is a reverse transcription (RT)-FOR primer which is used for the expression of adipocytes in differentiated immortalised human preadipose cells. This primer is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     Primer used for the expression of adipocytes in human preadipose cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human pre-adipose cell line capable of differentiating to adipose cells, useful in developing drug, food ingredients, and supplements against obesity, diabetes and cardiovascular diseases
                                                  1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 10; 30pp; English.
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                                                                                                                                                                                                                                                                    AAD29506 standard; DNA; 15 BP.
                                                                                                                                   1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                       15 AAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mace K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-188539/24.
                                                                      Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200206450-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Darimont C,
                  Sequence 15
                                                                                                                                                                                                                                                                                                                                               17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002
                                                                                                                                                                                                                                                                                                           AAD29506;
                                                      Query Match
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The invention relates to derivatised antisense oligoribonucleotides with enhanced membrane permeability and stability. The derivatised antisense configurabionucleotide complementary to a sequence of uncleotides found in a virus or a cell is useful for inhibiting e.g., viral reverse transcriptase. Derivatised antisense oligoribonucleotide is conjugated at the 2'-O position with a hydrophobic carrier reagent containing a poly substituted phenyl compound. The derivatised oligoribonucleotides are used to decrease the expression of cancer cells which rely upon oncogene expression for their phenotypic and pathological properties. The oligoribonucleotides are used for increasing the effectiveness of antisense oligonucleotide are also used for increasing the effectiveness of antisense oligonucleotide cargetted to a gene associated with a disease or a condition in an animal. To alter gene transcription and/or translation for any gene or gene segment responsible for expression of leukaemia virus, hepatitis virus, oncogenes and human immunodeficiency virus. The present sequence is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment which is used in the treatment of moloney murine leukaemia virus (MuLV)
                                                                                                                                   RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory; virucide; oncogene; cancer; transcription; translation; leukaemia virus; hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A]; poly-2'-0-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral reverse transcriptase comprises at the 2'-0 position of the oligoribonucleotide, a hydrophobic carrier reagent containing a poly substituted phenyl compound -
                                                                                               Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Column 24; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       93US-0022055.
94US-0200650.
96US-0604871.
                                                                                                                                                                                                                                                                                                                                                                   98US-0167375
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-009339/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WANG/) WANG J H.
                                                             12-FEB-2002
                                                                                                                                                                                                                                                                                      US6291438-B1
                                                                                                                                                                                                                                                                                                                                                                     06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1994;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                              18-SEP-2001.
                                                                                                                                                                                                                                              Retrovirus.
                     AAD22531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang JH;
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1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02; live 0; Mismatches 0; Indels 1084 AAAAAAAAAAAA 1098 15; Conservative Query Match Best Local Similarity Matches g ð

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Gaps

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1 AAAAAAAAAAAA 15

0

Gaps

· 0

0; Indels

1.4%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 3.5e+02;

100.0%; Preq.

Conservative

15;

Similarity

Query Match Best Local

Best Loca Matches

1084 AAAAAAAAAAA 1098

15 AAAAAAAAAAAA 1

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RESULT 777

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The present invention describes a method for cleaving single-stranded nucleic acid sequences at a desired location. Also described: (1) methods to displaying or expressing a member of a diverse family of peptides, collectively displaying at least a part of the diversety of the family, where the displaying at least a part of the diversity of the family, collectively displaying at least a part of the diversity of the family, an enchod for preparing single-stranded nucleic acids; (3) a method for preparing single-stranded nucleic genetic packages that display a member of a diverse family of peptides, polypeptides or proteins and that collectively display at least a portion of polypeptides or proteins and that collectively display at least a portion of the family; (4) a vector comprising a DNA sequence encoding an antibody variable region linked to a version of FILI anchor which does not mediate infection of phage particles, and wild-type gene III; (5) a method for producing a population or a library of immunoglobulin genes; and (6) a library of immunoglobulins that comprise members having at least one variable domain in which at least one of CDR1 and CDR2 contain synthetic diversity and CDR3 diversity is captured from B cells. The method is useful for cleaving single-stranded nucleic acid sequences at desired location, which can be subsequently used to produce libraries or genetic packages that display and/or express a diverse family of the present contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleaving single-stranded nucleic acid sequences at a desired location by contacting the nucleic acid with an single strand oligonucleotide complementary to a nucleic acid region where cleavage is desired -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoet R;
                                                                                                                                                                    Library; cleavage; display; diverse family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen EH, Nastri HG, Rookey KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 481; 485pp; English.
                  ABZ37501 standard; DNA; 15 BP
                                                                                                                                Oligonucleotide SEQ ID NO:622.
                                                                                                                                                                                                                                                                                                                                                             17-APR-2001; 2001US-0837306.
24-OCT-2001; 2001US-0000516.
25-OCT-2001; 2001US-0045674.
                                                                                                                                                                                                                                                                                                                         L7-APR-2002; 2002WO-US12405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOOGENBOOM H R J M.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      LADNER R C.
COHEN E H.
NASTRI H G.
ROOKEY K L.
HOET R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-093015/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ladner RC, Cohel
Hoogenboom HRJM;
                                                                                                                                                                                                                                                 WO200283872-A2.
                                                                                                                                                                                                                                                                                     24-OCT-2002,
                                                                                          18-FEB-2003
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                                                                                                                                                                                                             Synthetic.
                                                      ABZ37501;
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(COHE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROOK/)
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ABZ37501/c
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15 AAAAAAAAAAAA 1 엄

RESULT 778 ABV75865/

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New oligonucleotide deprotection reagent useful for deprotecting oligonucleotide comprises an active methylene compound and an amine reagent
                                                                                                    'note = "phosphoramidite linkage"
                                                                                                                       /mod_base= OTHER
/note= "3' Q-CDPI3"
                                                                           Location/Qualifiers
                                                  Deprotection; phosphoramidite; ss
                                                                                              'mod_base= OTHER
ВÞ
                                                                                                                                                                                08-MAR-2001; 2001US-274309P.
                                                                                                                                                                    04-MAR-2002; 2002WO-US06739.
                                      Oligonucleotide T15-Q-CDPI3.
ABV75865 standard; DNA; 15
                                                                                  1..15
/*tag= a
                         (first entry)
                                                                                                                 /*tag= b
                                                                                                                                                                                                                     WPI; 2003-046740/04.
                                                                                                                                                                                            (PEKE ) PE CORP
                                                                                                                                          WO200272864-A2.
                                                                            Key
modified_base
                                                                                                           modified base
                          05-FEB-2003
                                                                                                                                                       19-SEP-2002
                                                               Synthetic.
                                                                                                                                                                                                          Nelson J;
             ABV75865;
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Example 2; Page 25; 46pp; English.

oligonuclectide. This provinces a macrime of protected coligonuclectide, which is preferably covalently attached to a solid support through a linkage, with a deprotection reagent comprising an active methylene compound and an amine reagent comprising an active methylene compound and an amine reagent comprising an active methylene compound and an amine reagent. The process and reagent minimise side-reactions leading to certain impurities that contaminate synthetic oligonuclectides. The present sequence is a T15 phosphoramidite oligonuclectide having a quencher moiety (Q) and minor groove binder (CPP13) at this protected oligonuclectide and man symphole of the invention. This protected oligonuclectide was treated either with 15% ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that deprotection without DEM yielded a complex mixture of products containing only 26.5% of the desired product. When was used, 76.8% of the desired product was obtained. The present invention provides a method for deprotection of an

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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
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Gaps
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Query Match
1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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Gaps ., 0 Ξ

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15 AAAAAAAAAAAAA
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-protein coupled receptor; odourant; receptor; olfaction; array; droarray; anosmia; attractant; arometic; pesticide; PCR; primer;
                          Oligonucleotide used in cDNA library array.
      ABV74141 standard; DNA; 15 BP.
                   (first entry)
                   23-JAN-2003
                                 G-protein
            ABV74141;
RESULT 779
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/*tag= a /mod_base= OTHER /note= "5' polylinker" Location/Qualifiers Key modified_base Synthetic.

WO200277200-A2

5' End of cDNA library clone.

(first entry)

23-JAN-2003

03-OCT-2002.

26-MAR-2002; 2002WO-US09559

27-MAR-2001; 2001US-279168P. 31-JAN-2002; 2002US-353392P.

(INSC-) INSCENT INC.

Dimitratos S; Ď, Woods

WPI; 2003-029930/02.

Identifying nucleic acid encoding novel sex-linked-tissue-linked receptors, useful for isolating odcrant binding proteins or pessicide alternatives, by analyzing sequences from a male- and female-specific nucleic acid library -

Disclosure; Fig 5; 83pp; English.

The present sequence is that of a poly-T oligonuclectide used in a method designed to rapidly array and normalize a complex cDNA library obtained from a target species. Clones are arrayed into multi-well plates. Each well contains 16 oligonuclectides with a 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail and a unique 3' sequence, which allows an anchored oligonuclectide in each complementary 5' end. The unique 3' key sequences are designed to give a comprehensive level of degeneracy since they are diverse and numerous enough to ensure that every possible cDNA sequence can be bound by an individual, specific oligonuclectide in a single well. The CDNA library is heated to denature the clones into single stranded DNA, and an aliquot is added to every well. The anchored stranded DNA, and an aliquot is added to every well. The anchored cligonuclectide serves as the 3' primer in PCR, and the common 5' region present in every cDNA clone serves as the 5' priming site. Denaturing and washing leave anchored cDNA in each well. The library is now arrayed and normalised. The method was used to identify and cisolate clones encoding G-protein coupled receptors, especially colourant receptors, and active effectors involved in the olfactory proteins, or other olfactory or neuronal proteins. The identified reduce a target animal's sensitivity to odours, for manifacturing compounds or devices that mask odours, or trapping invertebrates with codourants. Semicochemicals (e.g. arometics or pheromone mimetics) can be developed with desirable effects on specific species, for the

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development of pest monitoring systems or non-toxic, species-specific pesticide alternatives, for controlling insect feeding and breeding behaviour, detecting the presence of small air-borne molecules, etc.
                                             Gaps
                                             0;
                                  Length 15;
                                            Indels
                           Score 15; DB 1; Len
Pred. No. 3.5e+02;
                     Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
                          Query Match 1.4%; Sco
Best Local Similarity 100.0%; Px
                                                      1084 AAAAAAAAAAAA 1098
                                                                                            ABV74142 standard; DNA; 15 BP
                                                                 15 AAAAAAAAAAAA 1
                                                                                                       ABV74142;
888666
                                                      ò
                                                                d
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G-protein coupled receptor; odourant; receptor; olfaction; array; microarray; anosmia; attractant; arometic; pesticide; ss. 26-MAR-2002; 2002WO-US09559. 27-MAR-2001; 2001US-279168P. 31-JAN-2002; 2002US-353392P. Dimitratos S; (INSC-) INSCENT INC. WPI; 2003-029930/02. WO200277200-A2 03-OCT-2002. Synthetic. Woods D,

Identifying nucleic acid encoding novel sex-linked-tissue-linked receptors, useful for isolating odorant binding proteins or pesticide alternatives, by analyzing sequences from a male- and female-specific nucleic acid library

Disclosure, Fig 5; 83pp; English.

Doughtoners of the consure that every possible cDNA sequence can be bound by an individual, specific oligomolectide in a single well. The cDNA library is heated to denature the clones into single well. stranded DNA, and an aliquot is added to every well. The anthored oligomolectide serves as the 3' primer in PCR, and the common 5' region present in every CDNA clone serves as the 5' priming site. Denaturing and washing leave anchored cDNA in each well. The library is now arrayed and normalised. The method was used to identify and isolate clones encoding G-protein coupled receptors, especially oddourant receptors, and active effectors involved in the olfactory The present sequence is that of the 5' end of a cDNA clone isolated from a cDNA library e.g. a mosquito antenna library. A clone was isolated using a method designed to rapidly array and normalize a complex cDNA library obtained from a target species. Clones are arrayed into multiwall plates. Each well contains 16 oligonucleotides (see ABV74137) with a 5' polylinker, a poly-r run capable of binding cDNAs by their poly-A tail and a unique 3' sequence, which allows an anchored oligonucleotide in each well to selectively hybridise only to those cDNA clones with a complementary 5' end. The unique 3' key sequences are designed to give a comprehensive level of degeneracy since they are diverse and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X) mS' - (alpha)n-beta-N3', or (X)mS' - (gammal-k-deltea-N3', where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, gamma = thymine or cytosine;

N = adenine, guanine or tytosine or thymine; gamma = thymine;

K = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.
pathway of invertebrates and vertebrates, e.g. odourant binding proteins, or other olfactory or neuronal proteins. The identified receptors and proteins are useful for identifying compounds that reduce a target animal's sensitivity to odours, for manufacturing compounds or devices that mask odours, or trapping invertebrates with odourants. Semicohemicals (e.g. arometics or pheromone mimetics) can be developed with desirable effects on specific species, for the development of pest monitoring systems or non-toxic, species-specific pesticide alternatives, for controlling insect feeding and breeding behaviour, detecting the presence of small air-borne molecules, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides having at least two new nucleotides - useful as primers in
                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                          Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT-PCR primer of the invention SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                         1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                                          Cuery Match
Best Local Similarity 100.00
Thes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX18368 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 781
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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X) m5 - (alpha)n-beta-N3', or (X)m5' - (gamma)k-delta-N3'; where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

N = adenine, guanine, cytosine or thymine; gamma = thymine;

k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guannine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for
                                                                                                                                                                              RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          - useful as primers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reproductive and highly efficient analysis of gene sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 1; Le
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                        Peptides having at least two new nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 other;
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                                                                                                                                                     RT-PCR primer of the invention SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 10; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular beacon target sequence.
                                                                     BP.
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                                                                 AAX18369 standard; DNA; 16
 TAAAAAAAAAAA 1
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                                                                                                                          (first entry)
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Best Local Similarity 100.(
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL57075 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                  (TAKI ) TAKARA SHUZO
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-183822/16.
                                                                                                                                                                                                                                     JP11032765-A
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                                                                                                                                                                                                                                                                                             18-JUL-1997;
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                                                                                                                          11-MAY-1999
                                                                                                                                                                                                           Synthetic.
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                                                                                              AAX18369;
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                                                                                                                                                                                                                                                                                                                                                                                                                     RT-PCR
                                          RESULT 782
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                                                     AAX18369,
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1.4%; Score 15; DB 1; Length 16; 100.0%; Pred. No. 3.8e+02; Live 0; Mismatches 0; Indels

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme, hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 40+02; O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 1 A; 1 C; 0 G; 15 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Escobedo J, McSwiggen J, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.10,0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 79; 218pp; English.
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95US-0005974.
                                                                                                                                                          96WO-US17480.
                                                                                                                                                                                                                       96US-0584040.
95US-0005974.
                                                                                                                                                                                                                                                                                                                                                    RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 AAAAAAAAAAAAA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-259017/23
                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP
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26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                              WO9715662-A2.
                                                                                                                                                          25-OCT-1996;
                                                                                                                                                                                                                       11-JAN-1996;
26-OCT-1995;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a perfectly matched target sequence for a molecular beacon comprising an oligonucleotide probe (see ABL57069) covalently attached at the 3' end to fluorescent dye and at the 5' end to a nanoparticle. In the native state, the proximity of the fluorence and quencher (gold nanoparticle) in the molecular beacon results in little or no detectable fluorescence. Upon hybridisation of the central complementary stretch of the probe to a target sequence, such as the present sequence, the hairpin undergoes a conformational change resulting in an increase in fluorescence, the extent of which is proportional to the amount of target sequence present. Single mismatches can be detected. The invention relates generally to the use of metal curface quenchers such as particles or films for high sensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flk-1, KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
                                                                                                 /*tag= a
/bound_moiety= "Molecular beacon"
/note="forms double-stranded region with bases
5-21 of sequence in ABLS7069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   applications in, for example, detection and diagnostic systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human flt1 VEGF receptor hammerhead ribozyme substrate #1094
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 15 A; 0 C; 1 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calame M, Libchaber A;
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 30; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2001; 2001WO-US41941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2000; 2000US-228728P.
30-MAR-2001; 2001US-280350P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-401727/43.
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                                                                          misc_binding
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RESULT 784 AAX69799,

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Gaps .,

16:51:41 2004

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Thu Jan

6

Gaps

0;

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

and treating IgA nephropathy.

SXS

Stinchcomb D;

Pavco P,

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(RIBO-) RIBOZYME PHARM INC
                                         Escobedo J, McSwiggen J,
                                                                                       WPI; 1997-259017/23,
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Sequence 17 BP; 0 A; 2 C; 0 G; 15 U; 0 other; Query Match Best Local Similarity 100.0 Matches 15; Conservative à

1084 AAAAAAAAAAAA 1098

AAV37934; RESULT 786 AAV37934/

WO9824815-A1 11-JUN-1998 Synthetic.

96JP-0325752 05-DEC-1996;

Nishi T; S, Takei Nagase T, Nakagawa S, Nie I, Sakurada M, Sawada S, Kuga T, Na Nomura N, Ishiwata T, Nishimura A,

PCR primers AAV37933-39 are used in the course of the invention. The specification descibes a novel protein isolated from leukocytes of patients with IgA nephropathy. Oligonucleotides based on the DNA sequence encoding this protein are useful as reagents for diagnosing Example 2; Page 33; 41pp; Japanese.

; 0 The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGP). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid archritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention. Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient Gaps 0; 1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4e+02; ative 0; Mismatches 0; Indels Length 17; Claim 4; Page 79; 218pp; English.

15 AAAAAAAAAAAA 1

AAV37934 standard; cDNA; 17 BP.

05-OCT-1998 (first entry)

Primer of the specification

Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.

97WO-JP04469 05-DEC-1997;

(KAZU-) KAZUSA DNA RES INST FOUND. (KYOW) KYOWA HAKKO KOGYO KK.

WPI; 1998-333259/29

and DNA encoding it - useful as reagents for IgA nephropathy Protein from leukocytes diagnosing and treating

This oligo(T) synthetic oligonucleotide was used for first strand cDNA synthesis from total RNA isolated from either logarithmically growing or quiescent 10T1/2 mouse fibroblast cells. It was also used with an arbitarary d(N10) primer in PCR. The PCR products were used in a differential display to identify the mSARP1 gene (see AAV19112) that codes for novel murine secreted apoposis related polynucleotides (see also ANW37814). The invention relates to SARP polynucleotides (see also ANW37815-17), antibodies specific for SARP, and use of such polynucleotides and antibodies in diagnostic and therapeutic methods, and methods for treating diseases related to the regulation of SARP expression in tissue and body fluid samples, New secreted apoptosis-related proteins - useful for modulating apoptosis, particularly for treatment of prostatic or breast cancer, also for diagnosis and monitoring of disease Secreted apoptosis-related protein; SARP; mSARD1; mouse; prostate cancer; breast cancer; diagnosis; gene therapy; PCR; 1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4e+02; Live 0; Mismatches 0; Indels 1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0; Indels Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other; Example 1; Page 30; 101pp; English. 1084 AAAAAAAAAAA 1098 AAV19118 standard; DNA; 17 BP. (LXRB-) LXR BIOTECHNOLOGY INC. 1084 AAAAAAAAAAAA 1098 96US-0028363. 96US-0026603. 97WO-US17154. 16 AAAAAAAAAAAA 2 (first entry) Query Match
Best Local Similarity 100.
Matches 15; Conservative Anchored oligo(T) primer. s, Conservative Query Match Best Local Similarity Thes 15; Conserve WPI; 1998-230704/20. including cancers. WO9813493-A2 24-SEP-1997; 11-OCT-1996; 24-SEP-1996; Melkonyan H, 28-AUG-1998 02-APR-1998 primer; ss. Synthetic. AAV19118; RESULT 787 AAV19118/c ద à d à

15 AAAAAAAAAAAA 1

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Gaps

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AAC64163;

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Pollenosis-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates
                                                                        PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
                                                                                            Human, pollinosis-associated gene 581, IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression, detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                       Obayashi M,
                                                                                                                                                                                                                                                     Kashiwabara T, Oshida T, Obay
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        Example 6; Page 40; 69pp; Japanese.
                   AAC64162 standard; DNA; 17 BP.
                                                                                                                                                                                           26-APR-2000; 2000WO-JP02732.
                                                                                                                                                                                                               99JP-0120492.
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolation of
                                                                                                                                                                                                                                                   Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                WPI; 2000-687341/67.
                                                                                                                                                    WO200065048-A1
                                                                                                                                                                                                              27-APR-1999;
                                                       21-FEB-2001
                                                                                                                                                                                                                                                    Nagasu T, S
Obayashi I,
                                                                                                                                                                       02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17
                                                                                                                                    Synthetic,
                                     AAC64162;
RESULT 788
          AAC64162/
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Gunji S;

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exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific Egy (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis-associated gene 581, to expression constructs and host cells comprising pollinosis-associated gene 581 to expression nucleic acids; pollinosis-associated gene 581 primers and probes; or pollinosis-associated gene 581 primers and probes; of pollinosis-associated gene 581 modeled of displayments of allergic diseases via the detection of pollinosis-associated gene 581 modeled and method of displayed associated gene 581 modeled of encoded of method of careening drug candidates for the treatment of pollinosis-associated consension of pollinosis-associated gene 582 modeled and method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen control-pollinosis-associated gene 581 is useful in the diagnosis control-pollinosis-associated gene 581 is useful in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss. The present sequence represents a PCR primer human pollinosis-associated gene 581 cDNA.
The invention relates to the human pollinosis-associated gene 581 which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a control Pollinosis-associated gene 581 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR prime
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Gaps
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o
1.4%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
                                 Conservative
              Local Similarity
16s 15; Conserv
Query Match
               Best Loca
Matches
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1084 AAAAAAAAAAA 1098 AAAAAAAAAAAA 16

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RESULT 789 AAC64163/c ID AAC64163 standard, DNA, 17 BP.

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Gunji S;
                                PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
                                              Human, pollinosis-associated gene 581; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                              Obayashi M,
                                                                                                                                                            Kashiwabara T, Oshida T, Obaya
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                  99JP-0120492.
                                                                                                                   26-APR-2000; 2000WO-JP02732.
                    (first entry)
                                                                                                                                              (GENO-) GENOX RES INC.
                                                                                                                                                           Nagasu T, Sugita Y,
Obayashi I, Imai Y,
                                                                                                                                                                                 WPI; 2000-687341/67.
                                                                                       WO200065048-A1.
                  21-FEB-2001
                                                                                                                                27-APR-1999;
                                                                                                     32-NOV-2000.
                                                                          Synthetic.
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The invention relates to the human pollinosis-associated gene 581 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgB (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis-associated gene 581; to expression constructs and host cells comprising pollinosis-associated gene 581 primers and probes; outleic acids; pollinosis-associated gene 581 primers and probes; anticleic acids pollinosis-associated gene 581 primers and probes; of pollinosis-associated gene 581 mucleic acids; plinosis-associated gene 581 primers and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 581 mucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen and anticle of a cells in the presence of a test compound relative treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 581 cDNA. to a control.Pollinosis-associated gene 581 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR prime

Pollenosis-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 40; 69pp; Japanese.

Gaps .. Length 17; Indels Score 15; DB 1; Le: Pred. No. 4e+02; 0; Mismatches 0; Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other; 1.4%; Scc. 100.0%; Pre 0; / Query Match
Best Local Similarity 100...
Best Local Similarity 100...

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1084 AAAAAAAAAAAA 1098 16 AAAAAAAAAAAAAA RESULT 790

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The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific 19E (immunoglobhlin E) levels. The gene with high cedar pollen-specific 19E (immunoglobhlin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen can be detection of pollinosis-associated gene 513 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 513 nucleic acids; and methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 513 in pollen antigen-stimulated companies of a test compound relative to a control.

T-cells in the presence of a test compound relative to a control.

Pollinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer control.

Control of the present sequence represents a PCR primer control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                          Gunji
PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
                                      Human, pollinosis-associated gene 513; IgE; immunoglobulin E, cedar pollen allergy, T-cell; reduced expression; detection, diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                   Kashiwabara T, Oshida T, Obayashi M,
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 38; 46pp; Japanese.
                                                                                                                                                                                                                                                        26-APR-2000; 2000WO-JP02733
                                                                                                                                                                                                                                                                                                   99JP-0120491
                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOX RES INC.
                                                                                                                                                                                                                                                                                                                                                                                 Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-687342/67.
                                                                                                                                                                   WO200065049-A1
                                                                                                                                                                                                                                                                                                27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                 Nagasu T, S
Obayashi I,
                                                                                                                                                                                                             02-NOV-2000
                                                                                                                           Synthetic.
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Gaps
                                         .
   1.4%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.(
Matches 15, Conservative
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AAC64173 standard; DNA; 17 BP. (first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.

Human, pollinosis-associated gene 513; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

WO200065049-A1.

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The invention relates to the human pollinosis-associated gene 513 which withhits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoslobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen consists of detection of pollinosis-associated gene 513 mucleic acids, a method of diagnosis of allergic diseases via the detection of pollinosis associated gene 513 mucleic acids, and methods of screening cut method of pollinosis associated gene 513 in ucleic acids, and methods of screening consists of allergic disease by measuring the caturage for the treatment of allergic disease by measuring the caturage and in the presence of a test compound relative to a control.

Collinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 513 cDNA.
                                                                                                                                                                                                                                                                                               Pollinosie-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                   Gunji S;
                                                                                                                                                                                              Obayashi M,
                                                                                                                                                                                          Kashiwabara T, Oshida T, Obay.
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 39; 46pp; Japanese.
                                                            26-APR-2000; 2000WO-JP02733.
                                                                                                         99JP-0120491
                                                                                                                                                   (GENO-) GENOX RES INC
                                                                                                                                                                                            Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                           WPI; 2000-687342/67.
                                                                                                         27-APR-1999;
                                                                                                                                                                                            Nagasu T, Si
Obayashi I,
                        02-NOV-2000.
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., Score 15; DB 1; Length 17; Pred. No. 4e+02; 0; Mismatches 0; Indels 100.08; PIC Local Similarity 100. Les 15; Conservative Query Match Matches

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Gaps

1084 AAAAAAAAAAAA 1098 16 AAAAAAAAAAAA g à

PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation. Human; pollinosis-associated gene 419; FAF-1 homologue; Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. (first entry) 21-FEB-2001 Synthetic. AAC64182;

BP.

AAC64182 standard; DNA; 17

RESULT 792 AAC64182/c

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26-APR-2000; 2000WO-JP02729. WO200065045-A1. 02-NOV-2000. THE STATE OF THE S

99JP-0120490. (GENO-) GENOX 27-APR-1999;

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The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from Individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 419 has common the gene encoding human Fas-associated gene 419 has been encoding human Fas-associated gene 419 primers of the invention also relates to the protein encoded by pollinosis gene associated gene 419 protein encoded by pollinosis gene associated gene 419 protein encoded by the gene; methods and probes; antibodies against the protein encoded by the gene; methods of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 nucleic acids; pollinosis-associated gene 419 protein encoded by the gene; methods of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 in cleic acids. The invention additionally encompasses of methods of screening drug candidates for the treatment of allergic companies of pollinosis-associated gene 419 in the creatment of allergic companies of classes of allergic diseases and in the presence of a test compound diagnosis of allergic diseases and in the presence of a test compound for the treatment of allergic diseases and in the presence of a test compound for the treatment of such and incomparent encoded gene 419 is useful in the presence of a treatment of allergic diseases and in the presence of a treatment of allergic companies of allergic diseases and in the presence of a treatment of allergic for the treatment of annex and in the presence of a treatment of allergic companies of allergic diseases and in the presence of a treatment of allergic companies of allergic diseases and in the presence of a treatment of allergic companies of allergic diseases and in the presence of a treatment of allergic companies of allergic co
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                                                                                                                                          Pollinosis-associated gene 419 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene
                               Obayashi M, Gunji S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Fas-associated factor-1; IgE; immunoglobilin E;
cedar pollen allergy; T-cell; reduced expression; detection;
diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
                          Kashiwabara T, Oshida T, Obay
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                Example 6; Page 49; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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                          Sugita Y,
Imai Y,
                                                                                                WPI; 2000-687338/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200065045-A1
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                                               Obayashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2001
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                            Nagasu T,
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Matches
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The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar collent appecific 1gE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 419 has common also relates to the protein encoded by pollinosis gene common also relates to the protein encoded by pollinosis gene associated gene 419 nucleic acids; pollinosis-associated gene 419 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene; methods of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 nucleic acids; pollinosis-associated gene 419 nucleic acids. The invention additionally encompasses of methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 419 in the control. Pollinosis-associated gene 419 in the treatment of such diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents
                                                              Pollinosis-associated gene 419 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15; DB 1; Length 1,,; Pred. No. 4e+02;
   ĸ
   Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
   Ogawa K,
                                                                                                                               Example 6; Page 50; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Sco.
7 100.0%; Pre
 Yoshida N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AAAAAAAAAAAA
Imai Y,
                               WPI; 2000-687338/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1999;
Obayashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Gunji S;

Kashiwabara T, Oshida T, Obayashi M, Yoshida N, Ogawa K, Matsui K;

(GENO-) GENOX RES INC.

Sugita Y, , Imai Y,

Nagasu T, S Obayashi I,

WPI; 2000-687339/67.

Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

Nagasu T,

Pollinosis-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 70; 80pp; Japanese.

The invention relates to the human pollinosis-associated gene 373 which with high cedar poller specific Igs (immunoglobulin B) levels. The gene wath high cedar poller specific Igs (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen relates to the protein encoded by pollinosis gene 373; expression constructs and host cells comprising pollinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 373 mucleic acids; pollinosis-associated gene 373 mucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 373 mucleic acids; and a method of gene 373 nucleic acids. The invention additionally encompasses methods of gene 373 nucleic acids. The invention additionally encompasses methods of 20 screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 373 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 373 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 373 cDNA.

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Score 15; DB 1; Length 17; Pred. No. 4e+02; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%; Pr

ð g RESULT 795

AAC64204 standard; DNA; 17 21-FEB-2001 (first entry) AAC64204/

BP.

PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.

Human; pollinosis-associated gene 373; IgE; immunoglobulin B; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065046-A1.

02-NOV-2000

26-APR-2000; 2000WO-JP02730.

99JP-0120489 27-APR-1999;

(GENO-) GENOX RES INC.

Gunji S; Kashiwabara T, Oshida T, Obayashi M, Yoshida N, Ogawa K, Matsui K; Sugita Y, , Imai Y, WPI; 2000-687339/67. Nagasu T, S Obayashi I,

Pollinosis-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates

The invention relates to the human pollinosis-associated gene 373 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene CC was isolated from T-cells from individuals allergic to cedar pollen constructs and by the protein encoded by pollinosis gene 373; expression constructs and host cells comprising pollinosis-associated gene 373 constructs and host cells comprising pollinosis-associated gene 373 primers and probes; constructs and host cells comprising pollinosis-associated gene 373 primers and probes; contibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 373 mucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of pollinosis-associated gene 373 mucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 373 in pollen anigen-stimulated T-cells in the presence of a test compound relative to anigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 373 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the creatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 373 cDNA. Example 6; Page 70; 80pp; Japanese.

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

0; 1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity Matches

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Gaps

1084 AAAAAAAAAAA 1098 N 16 AAAAAAAAAAAAA

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Gaps

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AAC64214 standard; DNA; 17 RESULT 796 AAC64214

BP.

21-FEB-2001 (first entry)

AAC64214;

PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.

Human, pollinosis-associated gene 627; IgE; immunoglobulin E, cedar pollen allergy; T-cell; reduced expression, detection, diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065051-A1

02-NOV-2000.

26-APR-2000; 2000WO-JP02735.

99JP-0120493 27-APR-1999;

(GENO-) GENOX RES INC.

Ω •• Gunj i T, Oshida T, Obayashi M, Ogawa K, Matsui K; Kashiwabara Yoshida N, Sugita Y, , Imai Y, Obayashi I, Nagasu T,

WPI; 2000-687344/67.

Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 42; 51pp; Japanese.

The invention relates to the human pollinosis-associated gene 627 which

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exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of dispnosis of allergic diseases wis the detection of pollinosis-associated gene 627 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 627 nucleic acids; and a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-55555555555555555

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Gaps ÷ DB 1; Le., 7. 46+02; 0; Indels 1.4%; Score 15; DB 100.0%; Pred. No. 4ettive 0; Mismatches Query Match Best Local Similarity 100. Matches 15; Conservative

1084 AAAAAAAAAAAA 1098

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Ŋ 16 ААААААААААААА

RESULT 797 AAC64215/c

AAC64215 standard; DNA; 17 BP

AAC64215;

(first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.

Human, pollinosis-associated gene 627; IgE; immunoglobulin E, cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic

WO200065051-A1.

02-NOV-2000.

26-APR-2000; 2000WO-JP02735.

99JP-0120493 27-APR-1999;

(GENO-) GENOX RES INC.

ŝ Gunji T, Oshida T, Obayashi M, Ogawa K, Matsui K; Kashiwabara Yoshida N, Sugita Y, , Imai Y, Nagasu T, S Obayashi I,

WPI; 2000-687344/67.

Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 42; 51pp; Japanese.

The invention relates to the human pollinosis-associated gene 627 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 627 nucleic acids, a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 627 nucleic acids; and a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence

of a test compound relative to a control. Pollinosis-associated gene 627 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 627 cDNA.

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Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Gaps ·, Score 15; DB 1; Length 1.;
Pred. No. 4e+02; Query Match Best Local Similarity 100.0%; Pred. No. 4e+ Matches 15; Conservative 0; Mismatches

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1084 AAAAAAAAAAAA 1098

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16 дадададададада

RESULT 798

AAC64231

0

BP. AAC64231 standard; DNA; 17

AAC64231;

(first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.

Human, pollinosis-associated gene 795; vimentin homologue, IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression, detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065050-A1.

02-NOV-2000.

26-APR-2000; 2000WO-JP02734.

99JP-0120494. 27-APR-1999;

(GENO-) GENOX RES INC. (EISA) EISAI CO LID.

ŝ Kashiwabara T, Oshida T, Obayashi M, Gunji Yoshida N, Ogawa K, Matsui K, Takahashi E; Sugita Y, Imai Y, Nagasu T, Sı Obayashi I, Yokoi A;

WPI; 2000-687343/67.

Pollinosis-associated gene 795 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Page 45; Example 6; 73pp; Japanese.

The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis gene 795; to expression constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 795 primers and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic diseases by meanwring the exercise of allergic diseases by meanwring the averaging drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 795 is useful in the diagnosis of

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The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has completely with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis-associated gene 795, to expression constructs and host cells comprising pollinosis-associated gene 795, antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 795 nucleic acids, pollinosis-associated gene 795 nucleic acids. The invention additionally encompasses methods of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by messuring the expression of pollinosis-associated gene 795 in pollen conting the expression of pollinosis-associated gene 795 in pollen a control. Pollinosis-associated gene 795 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the control. Pollinosis-associated gene 795 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer
allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 795 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, pollinosis-associated gene 795; vimentin homologue;
19E; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
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Yoshida N, Ogawa K, Matsui K, Takahashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
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                                                                                                                                 Query Match 1.4%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                           Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                         AAC64232 standard; DNA; 17 BP.
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Obayashi I, Imai Y,
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used in the isolation of human pollinosis-associated gene 795 cDNA.
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                                                              ch 1.4%; Score 15; DB 1; Length 17; Similarity 100.0%; Pred. No. 4e+02; 15; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4e+02;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                          Human IgA nephropathy-associated cDNA primer #62.
                              Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
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Sawada S, Takei M, Shibata K, Furuya A;
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ID AAX9
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AAX82722

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This sequence represents a PCR primer used in the identification of a human pollenosis associated gene. The gene is highly expressed in individuals with high pollen-specific immungalobilin E (IgB) levels. The invention relates to the nucleotide sequence encoding the pollenosis associated protein, diagnosing pollenosis and screening candidate compounds for treating pollenosis. The gene can be used in diagnosing pollenosis, particularly cedar pollenosis, and screening candidate compounds for pollenosis treatment.
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                                                                                                                                                                                                                                                                                                                                       Gene highly expressed in patients with high cedar pollen-specific IgE levels, useful for diagnosing pollenosis, and screening candidate compounds for pollenosis treatment
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IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
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100.0%; Pred. No. 4e+02;
iive 0; Mismatches 0;
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Lu N, Ogawa K;
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Lu N, Ogawa K;
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Best Local Similarity 100...
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, Imai Y,
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, Imai Y,
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Obayashi I,
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                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel DNA sequences preferentially expressed in 19A nephropathy patients, and DNA sequences stringently hybridizing to them. Independent claims cover diagnostic reagents for 19A nephropathy incorporating the antisense sequences; the treatment of 19A nephropathy using the antisense sequences for mRNA inhibition; proteins associated with 19A nephropathy, containing sequences encoded by the DNA sequences; antibodies recognizing these proteins; the production of the proteins by culture of host cells transformed with DNA encoding them, diagnossic reagents for 19A nephropathy containing the antibodies; and compositions for the treatment of 19A nephropathy which contain the antibodies. The products of the invention can be used for the diagnosis and treatment of 19A nephropathy. This sequence represents a primer used in the isolation described in the method of the invention.
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Pred. No. 4e+02;
0; Mismatches 0; Indels
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                                                                                                                                                   IgA nephropathy-associated cDNA primer #63.
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Shibata K, Furuya A;
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                                          AAX82722 standard; DNA; 17 BP.
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                                                                                                                (first entry)
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Takei M,
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                                                                                                                                                                                                      human; primer; ss.
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Query Match

Matches

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AAA30180

RESULT 803 AAA30180/

Sawada S,

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This sequence represents a PCR primer used in the identification of a human pollenosis associated gene. The gene is highly expressed in individuals with high pollen-specific immunoglobulin E (IgE) levels. The invention relates to the nucleotide sequence encoding the pollenosis associated protein, diagnosing pollenosis and screening candidate compounds for treating pollenosis. The gene can be used in diagnosing pollenosis, particularly cedar pollenosis, and screening candidate compounds for pollenosis treatment.
                                                                                         Gene highly expressed in patients with high cedar pollen-specific IgE levels, useful for diagnosing pollenosis, and screening candidate compounds for pollenosis treatment
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WPI; 2000-317712/27
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Query Match
1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other; 1084 AAAAAAAAAAAA 1098 16 AAAAAAAAAAAA ò d

AAA25448 standard; DNA; 17 RESULT 804 AAA25448/

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946. (first entry) 19-JUL-2000 AAA25448;

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Homo sapiens

WO9954459-A2

28-OCT-1999

99WO-US08547. 19-APR-1999;

98US-0082404. 20-APR-1998; 23-JUN-1998;

(RIBO-) RIBOZYME PHARM INC

Bellon L; Karpeisky A, Haeberli P; McSwiggen JA, is T, Woolf T, Jarvis T, Beigelman L, Thompson JD, Beigelman Reynolds M, Zwick M, Matulic-Adamic J;

WPI; 2000-013248/01.

optionally cleave, target nucleic acids that interact, and sequences, used to treat cancer New

Claim 77; Page 79; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting

treated cells, or for other conditions associated with levels of osstrogen receptor. Because of the high selectivity for targeted RNA, (A) alterations he used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that targets, and as research reagents (for RNA, in the same way that modification endonucleases are used with DNA). The combination of harmories in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA26107 to AAAA26218 represent their corresponding target sequences. AAA26107 to AAAA6218 represent their corresponding target sequences. AAA26107 to AAAA6212 represent their corresponding target sequences. AAA26219 to AAAA6217 represent corresponding target sequences. AAA26219 to AAAA6271 represent corresponding target sequences and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

0; Score 15; DB 1; Length 1,, Pred. No. 4e+02; Pred. --rohes 0; Indels 1.4%; Scc. 100.0%; Pre Query Match Best Local Similarity 100.0 Matches 15; Conservative

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Gaps

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Gaps

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AAZ36740 standard; DNA; 17 BP. RESULT 80: AAZ36740/0

AAZ36740;

13-MAR-2000 (first entry)

Anchored oligo(dT) primer GT15G used for modified differential display.

Stimulus-regulated nucleic acid; sequence profile; nucleic acid level; differentially expressed nucleic acid; disease state; cancer; autoimmune disease; infectious disease; aging; developmental disorder; proliferative disorder; neurological disorder; toxicity; primer; treatment resistance; differential expression; drug discovery; growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

Synthetic

WO9955913-A2

04-NOV-1999

99WO-US09119. 27-APR-1999;

98US-0083331, 98US-0098070. 27-APR-1998; 27-AUG-1998; 04-FEB-1999;

CANCER CENT SIDNEY. (KIMM-) KIMMEL

Trenkle T; Welsh J, Mcclelland M,

WPI; 2000-086388/07.

Measuring expression of low abundance reduced complexity target nucleic acid molecules -

Example 3; Page 91; 187pp; English.

AAZ36739-41 represent oligo(dT) primers used for modified differential display, in the method of the invention. The specification describes a method for measuring the level of two or more nucleic acid molecules in a target. The method comprises contacting a probe with an axbitrarily or statistically sampled target and detecting the amount of specific binding of the target to the probe. The methods can be used to identify differentially expressed nucleic acid molecules associated with disease

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states, such as cancer, autoimmune disease, infectious disease, aging, developmental disorder, proliferative disorder or neurological disorder. Alternatively the methods can be used to assess the efficacy or toxicity of or a resistance to a treatment. Also the methods can be used to determine differential expression of nucleic acid molecules in response to a stimulus, e.g. a chemical, drug or growth factor (especially can also be used to determine co-regulated some pathogen. The methods can also be used to determine co-regulated genes that can be potential targets for drug discovery.
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Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

; 0 1.4%; Score 15; DB 1; Length 17; [00.0%; Pred. No. 4e+02; Ve 0; Mismatches 0; Indels 100.08; Fir Query Match Best Local Similarity 100.0 Matches 15, Conservative

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AAZ35714 standard; DNA; 17

BP.

AAZ35714;

anchor PCR primer SEQ ID NO:3. Murine gene

(first entry)

31-JAN-2000

Rare expressed gene; analysis; expression; nucleic acid sample; PCR primer; ss

Synthetic.

Mus sp.

EP959141-A2

24-NOV-1999

99EP-0109795 18-MAY-1999; 98JP-0153651

(HITA) HITACHI LTD

Okano Irie T, Kiyama M, E, Fujita Muramatsu T,

Ä

WPI; 2000-001284/01

Preparation of nucleic acid sample, useful for analysis of rare expressed genes

Disclosure; Page 11; 22pp; English.

The present invention describes a process for the preparation of a nucleic acid sample comprising: (a) providing a nucleic acid sample comprising: (a) providing a nucleic acid sample or nucleic acid sample or plurality of kinds of probes having a known sequence substantially complementary to a portion of sequence of the nucleic acid sample; (b) mixing and hybridizing the nucleic acid sample with probes; (c) subsequently recovering nucleic acid sample with probes; (c) nucleic acid sample having a plurality of species of sequences, and providing one or a plurality of kinds of probes having a known sequence or substantially complementary to a portion of sequence of the nucleic acid sample; (ii) mixing and hybridizing the nucleic acid sample with the probes; (iii) treating the product of (ii) with nuclease activity of an enzyme or the probe itself; and (iv) subsequently recovering the nucleic acid molecules not digested by the nuclease activity in (iii), or (I) providing a nucleic acid sample having a plurality of species of sequences and oligonucleorides primer having predetermined sequences for synthesizing DNA strands; (II) providing one or a plurality of kinds of

probes having a known sequence substantially complementary to a portion of a sequence of the nucleic acid sample having such a structure to prevent a polymerase reaction from its 3' end and a nuclease reaction from its 5' end; (III) mixing and hybridizing the nucleic acid sample with the primers and probes; (IV) executing polymerase chain reaction with the primers and probes; (IV) executing polymerase chain reaction nucleic acid molecules synthesized in (IV). The method is useful for the preparation of a nucleic acid sample for the analysis of rare expressed exemplification of the present invention. 8888888888888888

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

.. Score 15; DB 1; Lengl...
"red. No. 44+02;
"red. No. 1ndels 1.4%; Scc. 100.0%; Pre Query Match
Best Local Similarity 100.
Matches 15; Conservative

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Gaps

1084 AAAAAAAAAAAA 1098 16 AAAAAAAAAAAAA 2 g

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Gaps

RESULT 80 AAC82875/

AAC82875 standard; DNA; 17

BP.

AAC82875;

(first entry) 20-MAR-2001

Human pollinosis-associated gene 441 primer #2.

Pollinosis, pollinosis-associated gene 441; allergy, T cell; pollen scattering; antigen; primer; ss

Homo sapiens.

WO200073435-A1.

07-DEC-2000.

18-MAY-2000; 2000WO-JP03190.

99JP-0148783. 27-MAY-1999;

(GENO-) GENOX RES INC.

Gunji S; Obayashi M, Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K; Sugita Y, , Imai Y, Nagasu T, S Obayashi I,

WPI; 2001-061526/07.

Pollinosis-associated gene 441 which undergoes lower expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of cells to antigen stimulus

Example 6; Page 35; 42pp; Japanese.

This invention describes a novel nucleic acid molecule comprising a sequence (I) which undergoes significantly low expression in subjects after pollen scattering, and is useful in diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen.

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

1.4%; Score 15; DB 1; Length 1,,
100.0%; Pred. No. 4e+02; 1.4%, 100.0%; Pro Query Match
Best Local Similarity
Local 15; Conservative

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Gaps

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1084 AAAAAAAAAAA 1098

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This invention describes a novel nucleic acid molecule comprising a sequence (I) which undergoes significantly low expression in subjects after pollen scattering, and is useful in diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen.
                                                                                                                                                                                                                                                                                                                                                         Pollinosis-associated gene 441 which undergoes lower expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of cells to antigen stimulus
                                                                                                                                         Pollinosis; pollinosis-associated gene 441; allergy; T cell; pollen scattering; antigen; primer; ss.
                                                                                                                    Human pollinosis-associated gene 441 primer #3.
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                                                     AAC82876 standard; DNA; 17 BP
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                                                                                                (first entry)
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, Imai Y,
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                                                                                                                                                                         Homo sapiens
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Obayashi I,
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                                                                         AAC82876;
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Matches
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Gunji S;

Obayashi M, 11 K;

Kashiwabara T, Oshida T, Ob Yoshida N, Ogawa K, Matsui

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                 DB 1; Lens.
o. 4e+02;
0; Indels
Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
                            1.4%; Score 15; DB 100.0%; Pred. No. 4e+cive 0; Mismatches
                                     Local Similarity 100.
nes 15; Conservative
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1084 AAAAAAAAAAAA 1098

AAC91720 standard; DNA; 17 BP. (first entry) PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.

Human; pollinosis-associated gene 787; pollen allergy; T-reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic

Obayashi M, Gunji S; 11 K, Takahashi E; Pollinosis-associated gene 787 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus Kashiwabara T, Oshida T, Obayar Yoshida N, Ogawa K, Matsui K, 18-MAY-2000; 2000WO-JP03192. 99JP-0148785 (GENO-) GENOX RES INC. (EISA) EISAI CO LID. Sugita Y, Imai Y, WPI; 2001-032159/04. WO200073440-A1. Nagasu T, Su Obayashi I, Yokoi A; 27-MAY-1999; 07-DEC-2000.

The invention relates to the human pollinosis-associated gene 787 which exhibits significantly reduced expression in the T-cells of individuals after the pollen-scattering season, relative to expression levels in T-cells before the pollen-scattering season. The gene was isolated from T-cells from individuals allergic to pollen using the differential display method. The invention also relates to pollinosis-associated gene 787 primers and probes; method of detection of pollinosis-associated gene 787 primers and probes; method of detection of pollinosis-associated control additionally encompasses a method of fargening frug candidates in the treatment of allergic disease by measuring the expression of pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in the screening of drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in associated gene 787 in pollen antigen-stimulated facels in the screening of drug candidates for the treatment of such diseases and in the screening of expression of the present sequence represents a PCR primer used in the isolation of the treatment of such diseases. human pollinosis-associated gene 787 cDNA. Example 6; Page 40; 54pp; Japanese.

Gaps .. Length 17; Indels Score 15; DB 1; Len ; Pred, No. 4e+02; Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other; 100.0%; Prec. ... 1.4%; 15; Conservative Query Match Best Local Similarity Matches

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Пр à

RESULT 810

AAC91721 standard; DNA; 17 BP 27-MAR-2001 (first entry) AAC91721;

PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation. Human, pollinosis-associated gene 787, pollen allergy; T-cell, reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

WO200073440-A1 Synthetic.

07-DEC-2000. = 44

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The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in (AAC92291), that undergoes significantly low expression in subjects after pollen scattering, and is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The present sequence respensents a PCR primer which is used in an example from the present invention.
                                                                                                                                                                                             Pollinosis-associated gene 465 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus
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                                                          Kashiwabara T, Oshida T, Obayashi M, Gunji
Yoshida N, Ogawa K, Matsui K, Takahashi E;
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Yoshida N, Ogawa K, Matsui K, Takahashi
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100 0%; Pred. No. 4e+02;
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                                                          Sugita Y,
, Imai Y,
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Imai Y,
            (EISA ) EISAI CO LTD.
                                                                                                                                                   WPI; 2001-061528/07.
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Matches 15; Conserv
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Obayashi I,
Yokoi A;
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Obayashi I,
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              HARAK BAKAR KARAK 
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Ogawa K, Matsui K, Takahashi E;
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Yoshida N,
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  18-MAY-2000; 2000WO-JP03192
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, Imai Y,
                                                                                            RES INC
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                                                                                                               (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                       WPI; 2001-032159/04.
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                                                                                         (GENO-) GENOX
                                           27-MAY-1999;
                                                                                                                                                             Nagasu T, S
Obayashi I,
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The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in 4AC92291), that undergoes significantly low expression in subjects after pollen scattering, and its useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The present sequence represents a PCR primer which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of primer GT15C.
                              Example 6; Page 44; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 66; 83pp; Japanese.
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Best Local Similarity
' "haq 15; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-557789/62.
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ID AAH47127 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200165259-A1
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BP.

DNA; 17

Gaps

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1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4e+02; ive. 0; Mismatches 0; Indels

100.08; Pre-

Conservative

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The invention provides a method of diagnosis of allergies that involves: assaying the levels of expression of genes B1001, B1466, B1072 or B1151 in T-cells, and comparing them with the level of expression in healthy T-cells. The method is useful for diagnosing allergies, particularly atopic dermatitis. The present sequence represents a PCR primer used for analysis of the expression of the above genes.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B1153 expression in allergic disease related PCR primer GT15C.
                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; allergy; B1153; differential expression; antiallergic; a antiasthmatic; antiinflammatory; atopic skin inflammation; PCR;
                                                                                                                                     Score 15; DB 1; Length 1,,
Pred. No. 40+02;
--rnheg 0; Indels
                                                                                                                       Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
                                                                                                                                          1.4%; Scc...
100.0%; Pre
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                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                           AAAAAAAAAAAA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; ss.
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                                                                                                                                                                                                                                                                                                           815
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Saito

Matsui K,

Obayashi I,

Gaps

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DB 1; Length 17; 4e+02; hes 0; Indels

1.4%; Score 15; DB 100.0%; Pred. No. 4e+tive 0; Mismatches

Query Match
Best Local Similarity 100.0
Matches 15; Conservative

1084 AAAAAAAAAAAA 1098

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Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

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B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                               Saito
                                                                                                                                                                                                                                                                                                                                                                          Diagnosis of allergies including atopic dermatitis
                                                                                                                                                                                                                                                                                                                           Obayashi I, Matsui K,
                                                                                                                                                                                                                                                                                    (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                 Nucleotide sequence of primer GT15G.
                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 66; 83pp; Japanese.
                           BP.
                                                                                                                                                                                                                                     23-FEB-2001; 2001WO-JP01372.
                                                                                                                                                                                                                                                              02-MAR-2000; 2000JP-0061832
                          DNA; 17
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                           Oshida T,
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-557789/62
                        AAH47128 standard;
                                                                                                                                                                                      WO200165259-A1
                                                                                                                                                             Homo sapiens.
                                                                         30-NOV-2001
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                                                 AAH47128;
RESULT 814
              AAH47128,
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Gaps

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Length 17;

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Length 17;

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The present invention relates to a method for examining allergic diseases with intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is also examining allergic diseases, particularly atopic dermatitis, which is also applicable in screening candidate compounds for remedies. The present sequence is an anchor primer described in the exemplification
                                             The present invention relates to a method of examining allergic diseases which comprises comparing the expression level of gene B1153 in allergy patients with the expression level in healthy subjects. The method is useful for the treatment, prevention, diagnosis and study of allergic diseases including atopic skin inflammation and asthma. The present sequence is a PCR primer described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Allergic disease examination method related anchor primer SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allergic disease; allergy; antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for examining allergic diseases by differential display intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients
                                                                                                                                                                                          Score 15; DB 1; Length 17;
Pred. No. 4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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                     Example 6; Page 82; 102pp; Japanese.
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                                                                                                                                                                                 1.4%; bcc.
100.0%; Pre
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                                                                                                                                                                                                                                                     1084 AAAAAAAAAAAA 1098
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Best Local Similarity
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Takahashi
                                                                                                                                        invention.
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                                                                                                                                                                                                                                                                                     The present invention relates to a method of examining allergic diseases which comprises comparing the expression level of gene B1153 in allergy patients with the expression level in healthy subjects. The method is useful for the treatment, prevention, diagnosis and study of allergic diseases including atopic skin inflammation and asthma. The present sequence is a PGR primer described in the exemplification of the
                                                                                                                                                                                                  Examination of allergic diseases comprises detecting gene B1153 over-expressed in T cells of allergy patients for diagnosis treatment and investigation of atopic skin inflammation and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examination of allergic diseases comprises detecting gene B1153 over-expressed in T cells of allergy patients for diagnosis treatment and investigation of atopic skin inflammation and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human B1153 expression in allergic disease related PCR primer GT15G.
                                                                                                                                                 Tsujimoto
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Pred. No. 4e+02;
0; Mismatches 0; Indels
                                                                                                                                                Nagasu T,
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                Sugita Y,
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                 CHILDREN'S HOSPITAL
                                                                                                                                                                                                                                                              Example 6; Page 82; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Scor.
100.0%; Pre
                                                                                                                                              Oshida T,
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                                          21-DEC-2001; 2001WO-JP11286.
                                                                       2000JP-0389476
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                                                                                                  RES INC.
GEN NAT (
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antiasthmatic; antiinfl
                                                                                                                                             Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-713252/77.
                                                                                                                                                                        WPI; 2002-713252/77
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Best Local Similarity
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                                                                                                                JAPAN
                                                                                                    GENOX
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                                                                       21-DEC-2000;
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               27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                invention
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Best Loc Matches

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Examining allergosis, involves measuring the expression levels of a specific gene, and comparing it to the levels in the eosinophils of healthy control -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the eosinophils of a healthy person. The method is used for the examination of allergosis. The present sequence represents a PCR primer, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examining allergosis, involves measuring the expression levels of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 1; Length 17;
Pred. No. 4e+02;
0; Mismatches 0; Indels
                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; allergosis; eosinophil; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                       Human; allergosis; eosinophil; PCR; primer;
                                       Nucleotide sequence of PCR primer GT15C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of PCR primer GT15G.
                                                                                                                                                                                                                                                                         KENKYUSHO KK.
ONI BYOIN INCHO.
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KOKURITSU SHONI BYOIN INCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 17; 20pp; Japanese.
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                                                                                                                                                                                                       25-SEP-2000; 2000JP-0291316.
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Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                       GENOX SOYAKU KEN
KOKURITSU SHONI
                                                                                                                                                                                                                                                                                                                        WPI; 2002-439993/47
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                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2002
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        20-AUG-2002
                                                                                                                                                                        02-APR-2002,
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                                                                                                                                                                                                                                                                                       (KOKU-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for examining allergic diseases with intersectin 2 gene or a gene with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the cosinophils in a patient, and comparing the expression level with that in the cosinophils of a healthy individual. The method is for examining allergic diseases, particularly adoptic dermatitis, which is also applicable in screening candidate compounds for remedies. The present sequence is an anchor primer described in the exemplification
                                                                                                                                                                                                                                                               Allergic disease examination method related anchor primer SEQ ID NO: 4.
                        Gaps
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                                                                                                                                                                                                                                                                                              Allergic disease, allergy, antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for examining allergic diseases by differential display of intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients -
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100.0%; Pred. No. 4e+02;
ative 0; Mismatches 0; Indels
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagasu T,
 Pred. No. 4e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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Local Similarity 100.0%; Phes 15; Conservative 0;
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AAL47236/c
ID AAL47236 standard; DNA; 17 BP.
                                                1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 1000.
Matches 15; Conservative
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                                                                               16 АААААААААААА
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                                                                                                                                                                                                                                                                                                                                                Unidentified
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Sugita Y, Takahashi E

16

ð dd RESULT 819

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Gaps

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specific gene,

Query Match

Best Loca Matches

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Gaps

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Indels

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which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN99812-ABN99828, in the eosinophils in a patient and comparing the expression level with that in the eosinophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is a PCR primer described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also
                                                                                                                                                                                                                                                                                                                                                      Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to a method for examining allergic
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100.0%; Pred. No. 4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Human allergic disease related PCR primer SEQ ID NO: 20.
       4e+02;
0;
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                   Pred. No. 4e+
Mismatches
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in screening compounds
100.0%; Fr
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                                                                    1084 AAAAAAAAAAAA 1098
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                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                          16 АААААААААААААА
                                     Conservative
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               Best Local Similarity
Matches 15; Conserv
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ID ABK49635 standard;
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                              primer; ss.
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                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for examining allergic diseases which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN99912-ABN99228, in the eosinophils in a patient and comparing the expression level with that in the eosinophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for exemplification of the invention.
       and comparing it to the levels in the eosinophils of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                            The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the ecsinophiis of a healthy person. The method is used for the examination of allergosis. The present sequence represents a PCR primer, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
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4e+02;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human allergic disease related PCR primer SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 1;
                                                                                                                                                                                                                              Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
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                                                                                                                                                                                                                                                                      1.4%; Score 15; DB 100.0%; Pred. No. 4e+tive 0; Mismatches
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JAPAN GEN NAT CHILDREN'S HOSPITAL.
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                                                       Example 1; Page 17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applicable in screening compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                   Local Similarity
les 15; Conserv
                         healthy control
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WO200233069-A1 Homo sapiens.

primer; ss

25-APR-2002

15-AUG-2002

ABN99830;

ABN99830/c RESULT 821

dd à

13-OCT-2000;

Sugita Y,

Query Match

(GENO-) (NIGE-)

H;

Saito

Nagasu T,

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Gaps

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Length 17;

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Human, se; PCR; acetyltransferase, 20-90-05; allergic disease; primer; differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.

Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.

Fujishima T, Nagasu T, Isujimoto G;

Ogawa K,

Hashida R,

Takahashi E;

Sugita Y,

WPI; 2002-315738/35

(GENO-) GENOX RES INC. (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL. (EISA) EISAI CO LTD.

21-SEP-2001; 2001WO-JP08246. 25-SEP-2000; 2000JP-0291318.

WO200224903-A1. Homo sapiens.

28-MAR-2002.

Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission stage in eosinophils of patients, also applicable in screening

Example 1; Page 57; 72pp; Japanese.

candidate compounds for remedies

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The invention relates to a method for examining allergic diseases comprises determining the expression level of a gene containing, the human colbn appearing as ABK49633 which has bownlooy with acetyltransferases in the eosinophils of a patient and comparing the expression level with that in the eosinophils of a healthy individual (i.e. differential display). Also included are methods of screening for candidate compounds which affect the expression level of the gene or the activity of the protein encoded by the gene (including related proteins and mutants), the use of probes based on the gene sequence in the examination of allergic diseases, the use of reporter constructs in the screening of candidate compounds, a vector containing a tentral constructs in the screening of candidate compounds, a vector containing the transcription-controlling respon of the gene, cells transformed with the vector, an antibody against the protein and a model animal for lowering of expression intensity of the gene in eosinophils. The method is examining allergic diseases particularly atopic dermatitis which is also applicable in screening candidate compounds for remedies. Such method can be performed in high throughput, at low cost. The present sequence is a differential display PCR primer.
                                                    Human, ss. PCR, acetyltransferase, 20-90-05, allergic disease, primer,
differential display, eosinophil, antiallergic; atopic dermatitis,
GTISC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagasu T, Tsujimoto G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission stage in eosinophils of patients, also applicable in screening candidate compounds for remedies.
         Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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                                                                                                                                                                                                                                                                        21-SEP-2001; 2001WO-JP08246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-315738/35.
                                                                                                                                                                                    WO200224903-A1.
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugita Y, Ha
Takahashi E;
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The invention relates to a method for examining allergic diseases comprises determining the expression level of a gene containing, the human colva appearing as ABK49633 which has homology with a cetyltransferases in the eosinophils of a patient and comparing the axpression level with that in the eosinophils of a healthy individual (i.e. differential display). Also included are methods of screening for candidate compounds which affect the expression level of the gene or the activity of the protein encoded by the gene (including related proteins and mutants), the use of probes based on the gene sequence in the examination of allergic diseases, the use of reporter constructs in the sureening of candidate compounds, a vector containing a the transcription-controlling region of the gene, cells transformed with the vector, an antibody against the protein and a model animal for lowering of expression intensity of the gene in eosinophils. The method is examining allergic diseases particularly atopic dermatities which is also applicable in screening candidate compounds for remedies. Such method can be performed in high throughput, at low cost. The present sequence is a differential display PCR primer compounds to the present sequence is a differential display PCR primer compounds.
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Local Similarity 100.0%; P.
Les 15; Conservative 0;
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Matches
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Gaps

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1084 AAAAAAAAAAAA 1098

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AAAAAAAAAAAA 2

16

ABK49636 standard; DNA; 17

RESULT 824 ABK49636, (first entry)

15-JUL-2002 ABK49636;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                      Examining allergic diseases by differential display of genes showing different expression particularly increase in remission stage in
            Atopic dermatitis; ss; differential display; primer; PCR; eosinophil; allergic disease; antiallergic; dermatological; GTI5c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atopic dermatitis; ss; differential display; primer; PCR;
eosinophil; allergic disease; antiallergic; dermatological; GTISg.
                                                                                                                                                                                                                                                               Saito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15; DB 1; Length 17; Pred. No. 4e+02;
                                                                                                                                                                                                                                                              Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human atopic dermatitis cDNA related PCR primer GT15g.
                                                                                                                                                                                                                                                              Fujishima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                            (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 55; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; SCUL.
100.0%; Pre
                                                                                                                                                                                                                                                              Ogawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 AAAAAAAAAAA 1098
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                                                                                                                                                   21-SEP-2001; 2001WO-JP08247.
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                                                                                                                                                                               26-SEP-2000; 2000JP-0293021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                   eosinophils in patients -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                         Hashida R,
                                                                                                                                                                                                                                                                                       WPI; 2002-330097/36.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention
                                                                                       WO200226962-A1
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                                                                                                                    04-APR-2002
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                                                           Synthetic.
                                                                                                                                                                                                                                                           Sugita Y,
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comprising determining the expression levels of these genes and comparing the expression level with that in the eosinophils of a healthy individual. The method of the invention may have antiallergic or dermatological activities. The method can be used to diagnose allergic diseases particularly atopic dermatitis, and may also be used to screen candidate compounds for remedies. The method of the invention can be performed in high throughput, at low cost. The present sequence represents the GTISG PCR primer used to amplify the differentially amplified atopic dermatitis related cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POMPOUS;
                                                                                                                                                                                                                                               This invention relates to gene sequences that are differentially expressed in eosinophils from patients with atopic dermatitis in the increment stage as compared with those in the remission stage. These sequences are used in a novel method for examining allergic diseases
                                                                                                                                                           showing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPO Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Hunington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxis.
                                                                                                                                                     Examining allergic diseases by differential display of genes show different expression particularly increase in remission stage in ecsinophils in patients -
                                                                                               Saito
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Pred. No. 4e+02;
                                                                                             Nagasu T,
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                                                                                             Fujishima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
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                                            (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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100.0%; Pre
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                                                                                             Ogawa
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                26-SEP-2000; 2000JP-0293021
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ID ABX79793 standard; cDNA; 17
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                                                                                           Hashida R,
                                                                                                                         WPI; 2002-330097/36.
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les 15; Conserv
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                                                                                          Sugita Y,
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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for
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                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 15; Conservative
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apoptosis e.g. (monoclonal) antibodies for the protein, a in immunohistological staining, as apoptosis inhibitors. be used for treatment of apoptosis-related diseases.
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Matches
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                                                                                                                                                                                   repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeats in marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABN79676-ABX80022 are the polymorphic repeats identified for a search of human BSTS.
                                                                                                                                                                 The invention discloses a method for identifying a candidate polymorphic
                                 Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 40+02;
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                                                                                                                               Examples; Column 483; 588pp; English.
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                                                                                             polymorphic probability
WPI; 2003-208818/20.
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as a reagent . It can also
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                                                                                                                                                                                 Gaps
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                                                                                                                                 Length 18;
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Pred. No. 4.3e+02;
                                                                                   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
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1.4%; Score 15; UB
Best Local Similarity 100.0%; Pred. No. 4.3
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ID AAVS4174 standard; cDNA; 18 1
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AC AAVS4174;
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97WO-JP04216.
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AAV35391/c
ID AAV35391 standard; DNA; 18
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                                                                                                                                                                                                  15; Conservative
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(JAPG ) NIPPON ZEON KK.
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      WPI; 1998-495844/42.
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                                                                                                                                                        Sequence 18
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                        method
                                         PCR; primer, amplification, apoptosis, antibody, inhibition, ss;
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Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               Example 1; Page 50; 70pp; Japanese
                     Nucleotide sequence PCR primer 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence PCR primer 12
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21-DEC-1998 (first entry)
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                                                                                                                                        05-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1998
                                                                                                                    11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1998
                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV54175;
                                                                                                                                                                                                       Sakaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV54175/
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(KYOW) KYOWA HAKKO KOGYO KK

Sakaki Y;

97JP-0050302

05-MAR-1997;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus; vaccines; infection; protection; primer; ss.
                                                                                                    This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vaccinia virus containing fusion HIB gag gene - for production in host cells of gag protein for use as vaccine
Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis
                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                  1.4%; Score 15; DB 1; Lu
100.0%; Pred. No. 4.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                          BP; 0 A; 2 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAT INST INFECTIOUS DISEASES.
                                                              Example 1; Page 51; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 64; 84pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-1 gag protein DNA primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yasuda A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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BP.

AAA58386 standard; DNA; 18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used with a polynucleotide composed mainly of Thymine bases (AAA58386)
                                                                                                                                                                                                                                                                                                                                                                                                                          Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
                                                                                                                Gaps
                                                                                                              .,
 protecting against infection with retroviruses such as HIV.
                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide # 1 used in a biomolecule detection system.
                                                                           Length 18;
                                                                                                          Indels
                                                                     Query Match 1.4%; Score 15; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 other;
                                  Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castro S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 68; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      target analyte, forms dendrimer
amplify the fluorescent signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nelson MB,
                                                                                                                                                                                                                                                                             퍔.
                                                                                                                                               1084 AAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US26612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0107828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0437076
                                                                                                                                                                                                                                                                         AAA58385 standard; DNA; 18
                                                                                                                                                                                  18 AAAAAAAAAAAAA 4
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOC-) BIOCRYSTAL LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbera-Guillem E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200028088-A1
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                                                                                                                                                                                                                                                                                                                AAA58385;
                                                                                                                                                                                                                                        RESULT 833
SXS
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nonfotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of manocrystals, which have polynucleotides complementary to the first to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Thymine bases. This sequence may therefore be used with a polynucleotide composed mainly of Adanine bases (AAAS8385).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to functionalised nanocrystals for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adipose tissue, obesity, diabetes, hyperlipemia, hypertension, human, arteriosclerosis, hyperuricemia, sleep apnea syndrome, PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
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                                                                                                                                                                                                                        Polynucleotide # 2 used in a biomolecule detection system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Match 1.4%; Score 15; DB 1;
Local Similarity 100.0%; Pred. No. 4.3e+0
ies 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Castro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 69; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbera-Guillem E, Nelson MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target analyte, forms dendrimes amplify the fluorescent signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ90641 standard; DNA; 18 BP.
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99US-0437076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LO-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1998;
09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                  AAA58386;
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AAA58386/C

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Matches
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Gaps

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Length 18; 0; Indels

1.4%; Score 15; DB 1; Le 100.0%; Pred. No. 4.3e+02;

1.40, 100.0%; Fr.

Conservative

Local Similarity nes 15; Conserv

Best Loca Matches

Query Match

1084 AAAAAAAAAAAA 1098

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AAAAAAAAAAAA 18

RESULT 834

Mismatches

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(AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAX67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identification of genes and proteins of adipose
                                                                                                                                                                                                                                                                                                                                                                                                                             Adipose tissue, obesity, diabetes; hyperlipemia; hypertension; human, arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A physiologically active protein specifically derived from mammal tissue -
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                                                                                                    Score 15; DB 1; Length 10;
Pred. No. 4,3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                               Human adipose tissue gene amplifying primer #11.
                                                                                         Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
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                                                                                                           1.4%; Scc.
100.0%; Pred. No. ..
'.. 0; Mismatches
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                                                                                                                                                                                                                                                                                                 AAZ90650 standard; DNA; 18 BP
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                                                                                                                                                        Conservative
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                                                                                                                                      Local Similarity
nes 15; Conserv
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les 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1998;
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ID AAZ90
XX
AC AAZ90
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0
                                                                                                                                                                                                                                                                                             tissue relating to obesity, particularly complications of visceral possity including diabetes, hypertalpemia, hypertension.

arteriosclerosis, hyperturicemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAY50598-X67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
                                                                                                                                                                                                                                                                           The invention relates to identification of genes and proteins of adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                               physiologically active protein specifically derived from mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physiologically active protein specifically derived from mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 1.4%; Score 15; DB 1; Length 18; Similarity 100.0%; Pred. No. 4.3e+02; 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adipose tissue gene amplifying primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                             Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                 (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                 WPI; 2000-306578/27
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Best Local Similarity
Matches 15; Conserv
      JP2000037190-A.
                                                                                                   23-JUL-1998;
                                      08-FEB-2000
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                                                                                                                                                                                                                                                                                                                        tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AA230631-633) and the proteins (AAYF7598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AA296640-51 represent PCR primers amplifying the human adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, sinusitis; ulcerative colitis; nephritis; amyloidosis, sarcoidosis; rheumatoid arthritis; scleroderma, lupus; non-allergic rhinitis; polymyositis, Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing, enzyme;
                                                                                                                                                                                                                                                                                                                 The invention relates to identification of genes and proteins of adipose
                                                        Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               A physiologically active protein specifically derived from mammal tissue -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 5-lipoxygenase gene related DNA sequence SEQ ID No 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Le1 . 4.3e+02;
                              Kuman adipose tissue gene amplifying primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 15;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                          Example 2; Page 18; 50pp; Japanese.
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                                                                                                                                                              98JP-0225228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT11136 standard; DNA; 18
           13-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                           TOBACCO INC.
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                                                                                                                                                                                                                                WPI; 2000-306578/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                JP2000037190-A
                                                                                                                                                                                                          (NISB ) JAPAN
                                                                                                                                                              23-JUL-1998;
                                                                                                                                                                                    23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                  tissue genes
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2002
                                                                                                                                        08-FEB-2000
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The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-Lo) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, anrotides, ulcerative colitis, nephritis, amyloidosis, concentration arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-lipoxygenase (5-Lo) gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer, PCR, polymerase chain reaction, sequencing, walking, complementary extension reaction; low redundancy; universal primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                    New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 1; Le
Pred. No. 4.3e+02;
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100.0%; Pred. No. ---
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 2 A; 3 C; 9 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                               Claim 10; Page 237; 290pp; English.
                                        (MILL-) MILLENNIUM PHARM INC.
21-AUG-2001; 2001US-314248P.
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95JP-0238141.
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ID AAT73293 standard; DNA;
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                                                                                                                            WPI; 2002-627522/67.
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                                                                                   Meyer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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18-SEP-1995;
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                                                                                   Barnes G,
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simultaneous sequencing of restriction enzyme fragment and adjacent region of intact DNA, avoids the need for cloning and requires fewer primers
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Example 1; Page 23; 50pp; English.

A method for DNA analysis based on a complementary extension reaction using a DNA polymerase, comprises a combination of fragment walking and DNA sequencing. DNA fragments are formed by digestion of DNA with a restriction enzyme and the targeted DNA sequence can be determined directly from the digested DNA fragments. By exploring the overlapping sequence of the determined base sequence, the overlal base sequence of a lengthy DNA can be determined with low redundancy without cloning or subcloning. In addition, the method can be done with commercially existing methods. ANT3221-92 are primers used in determination of the public sequence. Primer extension was carried out using 16 primers AAT73293

Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 2 other;

·; Length 20; Indels DB 1; Ler 4.7e+02; thes 0; Mismatches Score 15; Pred. No. 1.4%; SCOL. 100.0%; Pre 15; Conservative Query Match Best Local Similarity Matches 15; Conserv

1084 AAAAAAAAAAAA 1098 AAAAAAAAAAAA 1 15 à

AAX32003 standard; DNA; 20 AAX32003; RESULT 841 AAX32003/c

BP.

gene specific primer. MSH2

(first entry)

14-JUN-1999

Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer; CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53; Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis; colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene; BAP1 gene; PCR primer; ss.

Synthetic

WO9906598-A2

04-AUG-1998; 11-FEB-1999

98US-0084471. 22-MAY-1998; 04-AUG-1997;

(ONCO-) ONCORMED INC

Murphy PD;

WPI; 1999-153820/13.

Ε. Determining common functional alleles in a population - useful the diagnosis of disease associated with allelic heterogeneity

Example 1; Page 24; 78pp; English.

The invention relates to methods of determining a functional allele profile of a gene in a population. Functional allele profiles comprise the commonly occurring alleles in a population, and the relative frequencies at which such alleles of a given gene occur. The methods are used to identify and determine the frequency of the functional

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alleles of genes which display extensive allelic heterogeneity, particularly those implicated in disease or conditions, such as the BRCA1 gene associated with breast cancer. CFTR associated with cystic fibrosis, dystrophin associated with Duchenne muscular dystrophy and Becker muscular dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can also be employed for diseases where allelic and genetic heterogeneity exist, such as breast cancer, Identification of hereditary non-polyposis colorectal cancer. Identification of functional alleles is necessary for identification of mutations which may be implicated in the disease. Sequences AAX3001-172 represent primers for determining the functional allele profiles of various genes. The primers are specific for genes such as MSH2 gene, MLH1 gene, BRCA1 gene,
                                                                                                                                                                                                                                                                                                                                                                          BRCA2 gene and BAP1 gene.
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Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;

; 0 Gaps 0; Length 20; Score 15; DB 1; Length 20; Pred. No. 4.7e+02; 0; Mismatches 0; Indels 1.4., 100.0%; Pr Query Match
Best Local Similarity 100.
Matches 15; Conservative

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Gaps

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RESULT 842 AAX32010/c

BP. AAX32010 standard; DNA; 20

AAX32010;

(first entry) 14-JUN-1999

MSH2 gene specific primer.

Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer; CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53; Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis; colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene; BAP1 gene; PCR primer; ss.

Synthetic.

WO9906598-A2

11-FEB-1999,

98WO-US16574. 04-AUG-1998; 98US-0084471. 97US-0905772. 22-MAY-1998; 04-AUG-1997;

(ONCO-) ONCORMED INC

Murphy PD;

WPI; 1999-153820/13

Determining common functional alleles in a population - useful in the diagnosis of disease associated with allelic heterogeneity

Example 1; Page 24; 78pp; English.

The invention relates to methods of determining a functional allele profile of a gene in a population. Functional allele profiles comprise the commonly occurring alleles in a population, and the relative frequencies at which such alleles of a given gene occur. The methods are used to identify and determine the frequency of the functional alleles of genes which display extensive allelic heterogeneity, particularly those implicated in disease or conditions, such as the BRCA1 gene associated with breast cancer, CFTR associated with cystic fibrosis, dystrophin associated with Duchenne muscular dystrophy and Becker muscular dystrophy, and p53 associated with Li-Fraumeni syndrome.

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The methods can also be employed for diseases where allelic and genetic heterogeneity exist, such as breast cancer, neurofibromatosis, and hereditary non-polyposis colorectal cancer. Identification of functional alleles is necessary for identification of mutations which may be implicated in the disease. Sequences AXX2001-172 represent primers for determining the functional allele profiles of various genes. The primers are specific for genes such as MSH2 gene, MLH1 gene, BRCA1 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel recognition system comprising at least region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recognition system; screening; identification; pharmaceutical; toxin;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant protection agent; toxin; venom; carcinogen; venom; teratogen;
herbicide; fungicide; pesticide; beta-actin; human; ss.
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                         1.4%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 teratogens, herbicides, fungicides or pesticides.
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                                                                                                                                                                  Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 other;
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AAC82908 standard; DNA; 20 BP.
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                                                                                                                               BRCA2 gene and BAP1 gene.
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                         Query Match
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This invention describes a novel recognition system comprising at least 1 recognition unit bound to a support, each recognition unit comprising integion A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure -
                                                                                                                                                                                                                   Recognition system; screening; identification; pharmaceutical; toxin; plant protection agent; toxin; venom; carcinogen; venom; teratogen; herbicide; fungicide; pesticide; beta-actin; human; ss.
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Pred. No. 4.7e+02;
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100.0%; Pred. No. *...
0; Mismatches
                                                                                                                                                                                         Human beta-actin derived oligonucleotide #2.
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 TTAAAAAAAAAAA 1096
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                                                                                                  AAC82909 standard; DNA;
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Best Local Similarity
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1.4%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 4.7e+02; ative 0; Mismatches 0; Indels

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Query Match Best Local Similarity Matches 15; Conserv

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                                                                                                                                                                                                                                                            Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure.
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Recognition system; screening; identification; pharmaceutical; toxin; plant protection agent; toxin; venom; carcinogen; venom; teratogen; herbicide; fungicide; pesticide; beta-actin; human; ss.
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Best Local Similarity 100.
Matches 15; Conservative
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This invention describes a novel recognition system comprising at least 1 recognition unit bound to a support, each recognition unit comprising region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaccuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides or pesticides.
                                                                          Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure -
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100.0%; Pred. No. 4.7e+02;
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Burgstaller P;
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Hoppe H,
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tes 15; Conserv
Boekenkamp D,
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identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
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4.7e+02;
thes 0; Indels
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00.0%; Pred. No.
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                                                                                                                                                             1.4%,
100.0%; Pre
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Best Local Similarity 100.0
Matches 15; Conservative
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I recognition unit bound to a support, each recognition unit comprising a region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening,
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                                                                                                                                    Recognition system; screening; identification; pharmaceutical; toxin; plant protection agent; toxin; venom; carcinogen; venom; teratogen; herbicide; fungicide; pesticide; beta-actin; human; ss.
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                                                                                                    Human S-9 derived oligonucleotide #3.
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BP.
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AAC82919 standard; DNA; 20
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Best Local Similarity 100.
Matches 15; Conservative
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Query Match 1.4%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.7e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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This invention describes a novel recognition system comprising at least I recognition unit bound to a support, each recognition unit comprising region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaccuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
                                                     Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure.
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Pred. No. 4.7e+02;
0; Mismatches 0;
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es 15; Conservative 0;
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                          WPI; 2001-050938/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-050938/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 852
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         comprising a
                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel recognition system comprising at least 1 recognition unit bound to a support, each recognition unit comprising region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaccuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
                                                                                                                                                                                                                                                                                                Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recognition system; screening; identification; pharmaceutical; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant protection agent; toxin; venom; carcinogen; venom; teratogen;
herbicide; fungicide; pesticide; beta-actin; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 4.7e+02; trive 0; Mismatches 0; Indels
herbicide; fungicide; pesticide; beta-actin; human; ss.
                                                                                                                                                                                                (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CO KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;
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                                                                                                                                                                                                                                   Burgstaller P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe H, Burgstaller P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human S-9 derived oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                                                                                                                                                                                                                  Examples; Fig 1; 8pp; German.
                                                                                                                                  99DE-1023966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   Hoppe H,
                                                                                                                                                                                                                                                                WPI; 2001-050938/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                 Boekenkamp D,
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                                                                DE19923966-A1
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                                Homo sapiens,
                                                                                                                              25-MAY-1999;
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                                                                                                 30-NOV-2000
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identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting hepatic cell proliferative disorder useful for detecting hepatocellular carcinoma comprises detecting a methylated CpG-containing glutathione-S-transferase nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, glutathione S-transferase pi, GSTP1, CpG island, diagnosis, hepatic cell proliferative disorder, liver cancer, anticancer, tumourigenesis, detection, PCR primer, ss.
                                                                                                                                                                                 ;
                                                                                                                                         Length 20;
                                                                                                                                     1.4%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
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                                                                                                BP; 2 A; 3 C; 2 G; 13 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tchou JC, Bakker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 83; Page 42; 64pp; English.
                                                                                                                                                                                                                    1082 TTAAAAAAAAAA 1096
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                                                                                                                                                                                                                                                           TTAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                     AAF87713 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                          l Similarity 100.
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200126536-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                Sequence 20
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                                                                                                                                                                                                                                                                                                                                                                                              AAF87713;
                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                    RESULT 853
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The present invention relates to genes located on the X-chromosome of mammals. These genes are specifically expressed in haploid cells of the testis and encoded amino acid sequences having homology with the amino acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences of the invention are used for gene diagnosis, discrimination of sex, separation of sperm, infertility treatment and chromosomal manipulation, especially in livestock. They are also used in gene therapy. The present DNA sequence is a PCR primer which is used for the identification of genes by differential display method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New X-chromosome gene expressed in haploid cells of the testis, useful for gene diagnosis, discrimination of sex, separation of sperm, infertility treatment and chromosomal manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                      Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis; sex discrimination; infertility treatment; chromosomal manipulation; sperm separation; gene therapy; PCR; primer; ss.
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                                                                                                                                                                                             HT15-C downstream PCR primer used for identification of genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 4; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kondo T;
                                                                                                       BP.
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1082 TTAAAAAAAAAA 1096
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                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2000; 2000JP-0303994.
                                                                                                      AAD35095 standard; DNA; 20
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                       19 TTAAAAAAAAAA S
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Les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawakami A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-354153/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV GUNMA.
                                                                                                                                                                                                                                                                                                                EP1195382-A2
                                                                                                                                                                25-JUL-2002
                                                                                                                                                                                                                                                                                                                                             10-APR-2002.
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                                                                                                                                 AAD35095;
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(UYGU-)
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Matches
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Gaps

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Query Match 1.4%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.7e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose transporter; GLUT10; insulin; chromosome 20012-13.3; human; glucose metabolism; single strand conformational polymorphism; PCR; type 2 diabetes; SSCP; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                    "forms double-stranded region with bases 1-20 of sequence in ABL57069"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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/tag= a
/bound moiety= "Molecular beacon"
/note= "forms double-stranded regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Libchaber A;
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 26; 62pp; English.
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                                                                                                                                                                                                                                                                                                    29-AUG-2001; 2001WO-US41941.
                                                                                                                                                                                                                                                                                                                                        29-AUG-2000; 2000US-228728P. 30-MAR-2001; 2001US-280350P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Calame M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-401727/43.
                                                                                                                                                                                                                             WO200218951-A2
                                                                                           Key
misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dubertret B,
                                                                                                                                                                                                                                                               07-MAR-2002
                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel glucose transporter gene and protein, designated GLUTIO. GLUT 10 is an insulin-responsive glucose transporter gene located in the type 2 diabetes linked region of chromosome 20012-13.3. The GLUT 10 polypeptide can be expressed by standard recombinant methodology. The GLUT 10 glucose transporter gene and protein are useful for studying and analysing biological processes of both glucose metabolism and type 2 diabetes. These are also useful in drug screening techniques, especially for screening modulators of glucose transporter activity or compounds having the ability to be transported across the cell membranes. Sequences ABL58290-315 represent primers specific for the various regions of the human GLUT 10 glucose transporter gene. Used in single strand conformational polymorphism (SSCP) analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; K-ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
                                                                                                                                                                                                                                                                                           New glucose transporter gene and protein, designated GLUT10, useful fostudying and analyzing biological processes of glucose metabolism and Type 2 diabetes, as well as for screening modulators of glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 4.7
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                            Fossey SC;
                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 52; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 GGAGCAACTTGGTGC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2001; 2001WO-US10958.
                                                                                                                     22-AUG-2001; 2001WO-US26184.
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                                                                                                                                                     31-AUG-2000; 2000US-0652292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                        (UYWA-) UNIV WAKE FOREST
                                                                                                                                                                                                                          Dawson PA,
                                                                                                                                                                                                                                                                                                                                                transporter activity
                                                                                                                                                                                                                                                           WPI; 2002-371828/40.
                                              WO200218621-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200179548-A2
                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene, used j
of the gene
                                                                                   07-MAR-2002
                                                                                                                                                                                                                          Bowden DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABI96929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 857
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15-MAR-2001

Kliman

Favis R,

Gerry NP,

Zirvi M,

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14-APR-2000; 2000US-197271P.

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(CORR ) CORNELL RES FOUND INC
      WPI; 2002-034366/04
    Barany
                                                      RESULT 858
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The present invention describes a method (M1) for designing capture of ignorucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridise with little mismatch, where coligonucleotide probes (II) will hybridise with little mismatch, where coligonucleotide probes (II) will hybridise with little mismatch, where coligonucleotide probes (II) will hybridise with little mismatch, where coligonucleotide is useful managed. The method is useful infectious agents and coling infectious agents and coling infectious agents and parasitic infectious agents of selected from Onchovarva volvulus, Entamobba histolytica and Dracunculus selected from Onchovarva volvulus, Entamobba histolytica and Dracunculus as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Comedinesis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Concer is specifically associated with a gene selected from BRCAl gene, cancer is specifically associated with a gene selected from BRCAl gene, concer is specifically associated with a gene selected from BRCAl gene, concer is specifically associated with a gene selected from BRCAl gene, concerns and infrared microscope and infrared microscope and infrared microscope) the support at the confident of paticical x sites and identifying if ligation of the oligonucleotide probesed to presence or absence of the target uncleotide sequences. ABI932074 to the present or absence of the target uncleotide sequences used in the exemplification of the presence or absence or absence or absence or absence of the concerns invention and the concerns invention and contracted and exemplification in the exemplification of the presence or absence and the concerns invention and concerns invention and concerns i Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch -Example 5; Fig 29; 300pp; English. of the present invention.

Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;

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., Score 15; DB 1; Length 20; Pred. No. 4.7e+02; 0; Mismatches 0; Indels عتط (\$0.00t ي (0 1.4%; Local Similarity 100. nes 15; Conservative Query Match Matches

AAF96192 standard; DNA; 21 AAF96192;

BP.

(first entry) 06-JUN-2001

Human gene single nucleotide polymorphism #953.

polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds. Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

Human; 88; primer; cytochrome P450 Al; CYP4501Al; UGT2B4; MDR1; PCR;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF;

Cytochrome Caceptor betal; ADBR1; arxyl hydrocarbon; ARNT; Catheppsin S; CTSS;

Cytocoxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

COX2; diazepam binding inhibitor; DBI; haematological;

COX2; hicothamanide-N-methyl transferase;

COX2; hicothamanide-N-methyl transferase;

COX2; hicothamanide-N-methyl transferase 2B7;

COX2BT; UDP-glucuronosyl transferase 2B7;

COX2BT; UDP-glucuronosyl transferase;

COX2BT; UDP-glucuronosyl tra

Histamine N-methyl transferase (HNMT) PCR Primer #4.

(first entry)

23-DEC-2002

ABS97669;

ABS97669 standard; DNA; 21 BP.

859 ABS97669

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Gaps

Homo sapiens.

Location/Qualifiers replace (11, A) Variation

/*tag= a /standard_name= "single nucleotide polymorphism"

Homo sapiens

WO200118250-A2

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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of
                                                                                                                                                                                                  McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                  Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 15; DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                Bolk S, Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                correlations to diseases. The present sequence the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ....
                                                                                                                                           BIOMEDICAL RES.
                                                                                                                                                                                                Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                Examples; Page 116; 242pp; English.
                                                                99US-0153357.
2000US-0220947.
2000US-0225724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 GCCAGCGCCAACCTG 362
                                                                                                                                         (WHED ) WHITEHEAD INST BIOME:
(MILL-) MILLENNIUM PHARM INC
                                07-SEP-2000; 2000WO-US24503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 GCCAGCGCCAACCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 15, Conservative
                                                                                                                                                                                                Gargill M,
                                                                                                                                                                                                                                  WPI; 2001-226749/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                            atherosclerosis
                                                                  10-SEP-1999;
26-JUL-2000;
                                                                                                      16-AUG-2000;
                                                                                                                                                                                                Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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WO200257410-A2

25-JUL-2002

28-NOV-2000; 2000US-0724389

28-NOV-2001; 2001WO-US44838

(DNAS-) DNA SCI LAB INC.

Hall J: Guida M, WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits

Example 13; Page 123; 714pp; English

This invention relates to the sequence of an isolated mucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CP4501A1), advancemented P50 A2 (CP4501A2), advancemented P50 A2 (CP4501A2), advancemented P50 A2 (CP4501A2), advanced P Polymorphic sequences in ADREL or CHMR2 are used to cancer for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered pulmonary, immunological or the prostate, in LTF for altered immunological or haematological or benchin in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a PCR primer used to amplify the sequences of the invention.

Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;

1.4%; Score 15; DB 1; Length 21; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels 15; Conservative Local Similarity Query Match Best Loca Matches

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Gaps

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1084 AAAAAAAAAAA 1098 AAAAAAAAAAAAA 17

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ABS97681 standard; DNA; 21 BP. ABS97681

ABS97681;

(first entry) 23-DEC-2002

Histamine N-methyl transferase (HNMT) sequencing Primer #4.

Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; addrenegic receptor betal; ADBR1; aryl hydrocarbon; AHR, MRP2; NRII2; aryl hydrocarbon; ARR, MRP3; NRII2; aryl hydrocarbon; ARNT; cathepsin S; CYG5 cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydroxylase 2; BPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; MADPH quinone oxidoreductase 2; NQC2; sulfotransferase thermolabile; STM; UDP-glucuronosyl transferase; UGT2BH2; urokinase receptor; uPA; multidrug resistance 1; lactotransferzin; orphan nuclear receptor; uPA; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pullmonary; immunological; sequencing.

Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US44838.

28-NOV-2000; 2000US-0724389.

(DNAS-) DNA SCI LAB INC

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genee e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder—related traits

Example 13; Page 124; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 Al (CYP4501A1), adrenergic receptor betal (ADBR1), cytochrome P450 Ol2E1 (CYP4501A1), adrenergic receptor betal (ADBR1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARN1), cathepsin S (CTSS), cyclooxgenae 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (ERM2), 5-lipoxygenae activating protein (FLAP), glutathione-S-transferase 12 (GST12), histanine-N-methyl transferase (HNMT), Kallikrein 2) KAK2, nicotinamide-N-methyl transferase (HNMT), NDPH quinone oxidoreductase 2 (NO22), sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 20 (UGT2B1), unltidrug resistance (UGT2B15), uroxinase receptor (UGT2B1), multidrug resistance (UMR1), lactotransferrin (LTF), multidrug resistance associated (UMRN1), chann nuclear receptor (NRI12), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR3, or CHMR5) sequence. The polymorphism in the human genes cited in the human genes cited in the human genes cited in the human genes of the difference of the polymorphism in the human genes cited in the content of the companion of the content of the conten characterising the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnoshing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained

RESULT 860

Page 378

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in CYP4501A1, CYPP4501A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2, MRI12, STW, UGT2E14, UGT2E15, AHR. MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2, AHR. MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 zer bused to screen for altered cardiovascular function, in CMZ2 for altered susceptibility to cancer. Colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered central nervous system haematological function, in KLZ2 for altered serine proctease activity in the prostate, in LTF for altered immunological or haematological thustion, in KLZ2 for altered serine protease activity in function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a sequencing primer used to sequence the polymorphic genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/*tag= a
/bound_moiety= "Molecular beacon"
/note= "forms double-stranded region with bases
/note= 121 of sequence in ABL57069"
                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                            Length 21;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                            1.4%; Score 15; DB 1; Le
100.0%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                           Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calame M, Libchaber A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 62; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular beacon target sequence.
                                                                                                                                                                                                                                                                                                                                          1084 AAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2001; 2001WO-US41941.
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                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL57071 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                           Query Match 1.43
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 861
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The present sequence is that of a perfectly matched target sequence for a molecular beacon comprising an oligonucleotide probe (see ABL57069) covalently attached at the 3' end to fluorescent dye and at the 5' end to a nanoparticle. In the native state, the

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invention, which contain a polymorphic base at position 24 of their nuclectide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human biallelic marker upstream amplification primer SEQ ID NO:7402.
probe forms a hairpin conformation with hybridised termini. The proximity of the fluorophore and quencher (gold nanoparticle) in the molecular beacon results in little or no detectable fluorescence. Upon hybridisation of the central complementary stretch of the probe to a target sequence, such as the present sequence, the hairpin undergoes a conformational change resulting in an increase in fluorescence, the extent of which is proportional to the amount of target sequence present. Single mismatches can be detected. The invention relates generally to the use of metal surface quenchers such as particles or films for high sensitivity applications in, for example, detection and diagnostic systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation;
amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ65654 to AAZ69578 represent human biallelic markers from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome; biallelic marker; high density disequilibrium
                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                           Score 15; DB 1; Lu; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                      Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                       100.0%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 1809; 2745pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAAAAAAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-013267/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 862
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ30373;
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ30373/c
   NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                     ó
                                                                                                                                                     Gaps
treatment.
N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
and 3367, are not actually given a sequence in the Sequence Listing from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       deoxyribonucleic acid; major groove; ethanoamino group; IL-1; aziridinylcytosine; cross-linking group; o-xyloso linking group; human interleukin-1 beta; inverted polarity region; ss.
                                                                                                                                                   ..
                                                                                                                   Length 18;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= f
/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "N-methyl-8-oxo-2'-deoxyadenine"
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note = "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                       Cross-linking oligomer 116 for targetting HUMIL1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.19
*tag=
1label= inverted polarity_region
note= "see comments"
                                                                                                                Score 14.8; DB 1;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
mod_base= OTHER
note= "N4N4-ethanocytosine"
                                                                              Sequence 18 BP; 9 A; 1 C; 7 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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mod_base= OTHER
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nod base= OTHER
                                                                                                                                                                                 117 AAACGGGAAGAAAGGATG 134
                                                                                                                                                                                                                AAACGAGAAGGAAGGATG 18
                                                                                                                                                                                                                                                                                                       BP.
                                                                                                              Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                     AAQ20030 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krawczyk S;
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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modified_base
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25-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc feature
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Gaps
                                                                                                                                                        This oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. Residues 13 and 14 are linked via an o-xyloso group (i.e. mucleotides that have xylose sugar linked via the o-xylene ring). The sequence is designed to target the Human interleukin-1 beta gene beginning at nucleotide 7378 and will covalently cross-link to it via the N4N4-ethanocytosine group. See also AAQ20026-Q20029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligomer HUM beta 113 for forming triplex with IL-1 target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= e
|mod_base= OTHER
'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
New sequence-specific non-photo-activated crosslinking agents bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. HIV
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'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/*tag= g
/note= "o-xyloso dimer synthon linkage"
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mod_base= OTHER
note= "OTHER= N6 methyl-8-oxo 2'
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2"
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88.9%; Pred. No. 4.9e+02;
iive 0; Mismatches 2;
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*tag= 1
|abel= inverted_polarity_region
note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                          Example 4; Page 25; 42pp; English.
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/mod_base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ30373 standard; DNA; 19
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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17-APR-1991; 17-APR-1991; 27-SEP-1991;

Froehler B,

18-JAN-1991; 08-APR-1991; 17-APR-1991;

25-NOV-1991;

23-NOV-1990

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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and othera like it are useful in a diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV; HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso formed from an o-xyloso dimer synthon. The linking may reader to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ3226-448.
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                                                                                                      'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/mod_base= OTHER
/mod_base= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
14..19
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/mod_base= CTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                    note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine
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/note= "o-xyloso dimer synthon linkage"
                       'note= "OTHER= N4 N4 ethanocytosine"
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label= inverted polarity_region
note= "see comments"
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                                                                                  OTHER
                                                                                                                                                                   OTHER
'mod_base= OTHER
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/mod_base=
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/mod_base=
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/*tag=
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                                       modified_base
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17-APR-1991;
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18-JAN-1991
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  The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions tumours and inflammation. The triple helices form of conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso funcleotides have the 3' positions of xylose sugars linked via the o-xylosuchene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthon. This additional modifications may render the bilgomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems.

(Updated on 25-MAR-2003 to correct PN field.)
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HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                            New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
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                                                                                                                                                                                                                                                                  Matteucci MD, Milligan J;
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88.9%; Pred. No. 4.9e+02;
ative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 70; 77pp; English.
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                                                                       910S-0643382.
910S-0683420.
910S-0686544.
910S-0686546.
910S-0686546.
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                 91WO-US08811
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(first entry)
                                                                                                                                                                                                                                                                Krawczyk S,
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Key modified_base

Synthetic.

25-MAR-2003 07-DEC-1992

AAQ30376;

RESULT 865

AAQ30376/

Query Match

Matches

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AAT04915-T04922 are oligonucleotide primers and probes used for the amplification and sequencing of mammalian stem cell factor (SCF).

Non-naturally occuring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally courring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for reating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow appasia nerve damage, infertility, intestinal damage or myelopoiniferative disorders. Antibodies may be raised against the peptides for use in the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells
                                                                        Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
                                                                                                          Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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90US-0537198.
90US-0573616.
90WO-US05548.
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                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosselman RA, Martin FH,
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-346090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                              16-OCT-1989;
11-JUN-1990;
                                                                                                                                                                                                                                                                                             04-OCT-1990;
                    25-MAR-2003
15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
15-MAY-1996
                                                                                                                                                                                                                                                                                                                                 11-0CT-1990;
                                                                                                                                                                                                                       EP676470-A1
                                                                                                                                                                                                                                                           11-0CT-1995
                                                                                                                                                                                    Synthetic.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 333
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim a method of transporting a nucleic acid deriv. accros a membrane which comprises using a receptor that uses salt bridgin, aromatic stacking, H bonding and chelation to recognise the nucleic acid deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the examples.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of synthetic RNA oligo which is a target nucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport of nucleic acid derivs. across membranes - using new receptors which use salt bridging, aromatic stacking, hydrogen bonding and chelation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 17; DB 1; Length 20; 0.0.0%; Pred. No. 2.1e+02; ve 0; Mismatches 0; Indels
                                                                                       1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel receptor; nucleic acid; transport; oligo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 other;
See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Updated on 25-MAR-2003 to correct PN field.)
                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Table 1, page 38; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usman N;
                                                                                                                                                                 1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                           AAQ58578 standard; RNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAAAAAAAAAAAAA 17
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Matches 17; Conservative
                                                                                                                         Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De MENDOZA J, Rebek J,
                                                                                                                                                                                                                                                                                                                                                                   (updated)
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                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        novel receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9404194-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1992;
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21-AUG-1994
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                                                                                                                                                                                                                                                                                                                               AAQ58578;
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                                                                                         Query Match
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AAT04917/c
ID AAT0491
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AAQ58578
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Non-naturally occuring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancial engraftment of bone marrow during transplantation or for bone marrow or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertlilty, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells
   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT04915-T04922 are oligonucleotide primers and probes used for the
                                                                                         Stem cell factor; progenitor; haematopolesis; SCF; anaemia; thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft; transplant; neoplasia; myelosuppression; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zsebo KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugga SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 12C; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0422383.
90US-0537198.
90US-0573616.
90WO-US05548.
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Best Local Similarity
Matches 17; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
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                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1990;
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28-SEP-1990;
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                                                                                                                                                                                                                                                                                  EP676470-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-JUN-1990
                                                                                                                                                                                                                       Synthetic
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The sequences represented by, AAQ90402-15 are synthetic DNA probes containing 5' amino termini. The sequences shown in AAQ90390-401 are synthetic DNA probes with 3' ribonucleoside termini. These sequences were specific for the polymorphisms of HLA gene dQs. The sequences were specific for the polymorphisms of HLA gene dQs. The sequences were specific for the polymorphisms of HLA gene dQs. The sequences were electronic device of the invention. This is a self-addressable electronic device (SAED) that can be used to carry out multi-step and multiplex reactions, such as nucleic acid hybridisations. The advantages of this method are that these reactions can be carried out with complete and precise electronic control, and that the rate, specificity and sensitivity of these reactions are greatly improved at
                                                                                                    aminolink2 Thymine; allows binding to any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                           New self-addressable electronic devices - used for multi-step and multiplex reactions such as DNA hybridisation(s), clinical diagnostics and bio:polymer synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide ligand; steroid hormone; hapten; immobilisation; immunodetection; estradiol; alpha-anomer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 41; 86pp; English.
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/mod_base= OTHER
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(first entry)
                                                                                       /*tag=
                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                WPI; 1995-185870/24.
                                                                                                                                                                                                                                                                      (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                    Tu E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        micro-locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
modified_base
                                                                                                                                                                                                          26-OCT-1994;
                                                                                                                                                                                                                                        01-NOV-1993;
                                                                         misc_feature
                                                                                                                                                  WO9512808-A1
                                                                                                                                                                              11-MAY-1995.
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24-AUG-1995
                                                                                                                                                                                                                                                                                                  Heller MJ,
                             Synthetic.
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ID AAQ9
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispessing each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
                                                                                                                                                             - by amplification of mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                           CDNA and gene expression - by ampl digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                     Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aggregate; restriction enzyme; ss.
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      93JP-0112515
                                           93JP-0112515
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                                                                                                                      WPI; 1995-018287/03
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Best Local Similarity
Matches 17; Conserv
    16-APR-1993;
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followed by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotides (AAQ94201-094205) were synthesised for use as ligands. The ligands are covalently linked to a hapten (esp. a steroid hormone) to form a conjugate which is then immobilised on a solid support for interaction with antibodies against the hapten. Nucleic acid ligands are less likely to be recognised by the antibodies than are peptide ligands and nucleic acids are also less likely to undergo intramolecular organisation which interferes with accessibility of the hapten to the antibodies. For immunodiagnosis of oserradiol, the active hapten osestradiol-6-carboxymethoxime-N-hydroxysuccinimide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                     b "the glycosidic bonds between nucleotides are all in the alpha-anomer form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assay device for hapten or its specific antibodies - comprises support having competitive reagent immobilised via nucleic acid ligand to improve orientation and accessibility
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"carries a group derived ffrom aminopropanediol"
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                                                                                                                                                                                                                                                                                                                                                                                                           Kurfurst R,
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les 17; Conservative
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CROS P.
KURFURST R.
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RESULT 336 AAQ75599/c

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seperate lanes. The method can be used to analyse gene expression

rapidly and easily

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Length 20; 0; Indels

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AA075547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction argyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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1 Similarity 100.0%; Pred. No. 2.1e+02;
17; Conservative 0; Mismatches 0; Indels
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1.5%; Score 17; DB 1; L
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0;
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AAQ75601 standard; DNA; 20 BP.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSSEQ files AAQ/7547-Q7759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                             Reverse transcription primer used in cDNA analysis technique.
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1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ7554-7075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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              Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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tive 0; Mismatches 0;
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ID AAQ75604 standard; DNA; 20
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A method for the analysis of cDNA comprises (a) preparing
                                                                                                                                                                                                       Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 other;
                                                                    (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                     Disclosure; Page 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                  aggregate; restriction enzyme; ss.
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Best Local Similarity 100.0
Matches 17; Conservative
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer, (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and, (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
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RESULT 346 AAQ75593/c

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
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                                                                              1084 AAAAAAAAAAAAAA 1100
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                                                                                                                                       AAQ75568/c
ID AAQ75568 standard; DNA; 20 BP.
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AAQ75569 standard; DNA; 20 BP.
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Best Local Similarity
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rapidly and easily.
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                                                                                                                                                                                                                                       aggregate;
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AAQ75569/C
ID AAQ755
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                 Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
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AAQ75570 standard; DNA; 20
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AAQ75573 standard; DNA; 20
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                                                                                                             RESULT 353
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                                                                               A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVIS47-07758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cNNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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amplification of mRNA
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CDNA and gene expression - by ampli digestion with restriction enzymes
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                                                     Disclosure; Page 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggregate; restriction enzyme; ss.
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AAQ75571/c
ID AAQ75571 standard; DNA; 20
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Matches 17; Conservative
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Analysis of
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
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Local Similarity 100.0%; Pred. No. 2.1e+02;
Ne 17; Conservative 0; Mismatches 0;
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17 AAAAAAAAAAAAAA
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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AAQ75574 standard; DNA; 20 BP.
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Matches 17; Conservative
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1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels

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and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of emplayed aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                       expression; reverse transcription; primer; cDNA;
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                                                                                                                                                              Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                    aggregate; restriction enzyme; ss.
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ID AAQ75560 standard; DNA; 20
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                                                                                                                                                                               A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
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16-APR-1993;
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This oligonucleotide is used in the DNA cloning strategies of the Mycobacterium vaccae antigens. The invention provides M. vaccae polypeptides that comprise an immunogenic portion of a soluble M. vaccae antigen, or a variant, where the antigen induces an immune response in patients previously exposed to a mycobacterium. Such M. vaccae polypeptides can be used in methods for enhancing non-specific immune response. The methods and products can be used for the detection, tresponse. The methods and products can be used by mycobacteria such as M. vaccae, M. avium or M. tuberculosis. The products also have the ability to induce cell proliferation and cytckine products also have interferon-gamma and interleukin-12 production) in T cells, B cells, or macrophages. They can be used for enhancing immune responses for use in vaccines or immunotherapy of infectious diseases
                                                                                        Mycobacterium vaccae, antigen, therapy; prevention, cytokine production; M. avium; M. tuberculosis; immune response enhancer; cell proliferation; mycobacteria infection; vaccine; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide separated by capillary affinity gel electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium vaccae polypeptides - used to develop products for in detection, therapy and prevention of mycobacteria infections as immune response enhancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capillary afinity gel electrophoresis; separation; polymer-gel;
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1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                            M. vaccae antigenic sequence hybridising oligo AD12.
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25-AUG-1998 (first entry)
                                                                                                                                                                                                    Mycobacterium vaccae.
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                                                                                                             Gaps
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human T-cell lymphotropic virus type 1; viral antigen expression; ss.
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                                                          Query Match 1.5%; Score 17; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 17; Conservative 0; Mismatches 0; Indels
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                     Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 other;
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Best Local Similarity 100.C
Matches 17; Conservative
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process using capillary affinity gel electricably charget malecules brocess using capillary affinity gel electricably charget molecules relates to selective separation of electrically charget molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer gel. Receptors for target molecules are covabently bound to the polymer. An electric field of at least 50 volts/cm is applied. The capillary tube is charged with the analytical mixture. In a first separation stage, the target molecules are covabently bound to the receptors and the remaining components are eluted, optionally whilst splitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the alfinity of the target molecules for the receptor is eliminated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for selective separation and/or determination of charged organic compounds, such as oligonucleotides, peptides or carbohydrates. It may be used, than brior art processes, especially in the case of complex biological analytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using standard methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium vaccae protein, antigen, T cell activation, cytokine, dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy, tuberculosis; leprosy, sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma; PCR primer; ss.
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                                                                                                                                                                                                                                                                                     Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for target molecules are bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterial 16S rRNA specific oligo AD12.
                                                                                                                                                                                                                                                                                                                                                                 Example D3; Page 25; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                             Paulus A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ11326 standard; DNA; 20 BP
                                                                                                                                 96CH-0001320
                                                                                             97WO-EP02647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                             Muscate A, Natt F,
                                                                                                                                                                       (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                   WPI; 1998-041763/04
                                                                                                                                   24-MAY-1996;
                                                                                             23-MAY-1997;
                                                         04-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ11326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 363
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The invention provides heat-killed Mycobacterium vaccae, or recombinant M. vaccae proteins. The M. vaccae proteins may be employed to activate considerable and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of discorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, capporiasis, atopic dermatitis, eczema, allergic contact dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss; cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic RNA sequence produced by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 1.5%; Score 17; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 2.1e+02; No. 2.17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Watson J;
                                                                                                                                                                                                                                                                                         Prestidge RL, Skinner MA, Tan P, Visser ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Enhancing immune response to an antigen
                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Page 177; 243pp; English.
                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX27533 standard; RNA; 20 BP.
                                                                                                                                                                         97US-0997080.
                                                                                                                                           98US-0205426
                                                                                                                                                             97US-0996624
                                                                                                                                                                                                                        98US-0156181
                                                                                                              98WO-NZ00189
                                                                                                                                                                                                          98US-0095855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma and melanoma
               Mycobacterium vaccae.
                                                                                                                                                                                                                                                                                                                       WPI; 1999-430163/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  areata,
                                              W09932634-A2
                                                                                                            23-DEC-1998;
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                                                                                                                                                                                                                           17-SEP-1998;
                                                                                                                                            04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999.
                                                                              01-JUL-1999
                                                                                                                                                                                           23-DEC-1997
                                                                                                                                                                                                          11-JUN-1998
                                                                                                                                                                          23-DEC-1997
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX27533;
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The invention relates to silyloxymethyl protected D- or L-ribonucleosides and their phosphonates (I), and silyloxymethyl halides (II). (I) are intermediates for synthesis of RNA-oligonucleotides with predetermined nucleotide sequence, particularly by machine synthesis. The groups specified above, apart from those on silyl, are those particularly for the cyanocthyl phosphoramidate coupling. Uses of the oligoribonucleotide products in diagnosis, therapy, and as research tools, are well known, and are not dealt with in detail. (II) is an intermediate for (I). The silyloxymethyl halide reagent is easy to prepare, and yields are high. Introduction of the silyloxymethyl group into the ribonucleoside is simple and rapid, and the acetal bond formed does not migrate, eliminating particularly the prior art problem of 2' to 3' isomerisation. The methylenedioxy group spacer between the silyl group and nucleoside is eliminating particularly the prior art problem of 2' to 3' isomerisation. The methylenedioxy group spacer between the silyl group and nucleoside linkages, enabling first, a range of choices for the silyloxy coupling. Purer products are therefore obtained than in prior art, and indian larger quantities and longer chains of oligoribonucleotides to the subhabelical and longer chains of oligoribonucleotides to
                                                                                                                                                                                                                                                                                   2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have high purity, use in machine synthesis of ribonucleic acids, enable longer oligonucleotide chain construction, and larger amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesised successfully, and in shorter times.
                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 25; 38pp; English.
                                                                                                                                                                                               Weiss PA;
98WO-EP05215.
                                                97CH-0001931.
                                                                                                                                                                                               Jenny L, Pitsch S,
                                                                                                                                                                                                                                             WPI; 1999-180963/15
                                                                                           (JENN/) JENNY L.
(PITS/) PITSCH S.
(WEIS/) WEISS P.A.
17-AUG-1998;
                                                18-AUG-1997;
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. 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 0 A; 0 C; 0 G; 20 U; 0 other; Conservative Local Similarity tes 17; Conserv Query Match Best Loca Matches

1084 AAAAAAAAAAAAA 1100 20 AAAAAAAAAAAAAAA

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AAA40448 standard; DNA; 20 BP AAA40448; RESULT 365 AAA40448/c

Electochemical detection method fixed probe DNA. (first entry) 13-NOV-2000

Electrochemical detection; glucose; cholesterol; urea nitrogen; bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood; plasma; serum; urine; lymph diagnosis; probe; ss.

Synthetic

12-JUL-2000

3P1018646-A2

07-JAN-2000; 2000EP-0100126

99JP-0001111. 06-JAN-1999; 24-MAY-1999;

(FUJF) FUJI PHOTO FILM CO LID

Takenaka S, Ogawa M,

WPI; 2000-444372/39.

Quantitative analysis of a biochemical compound such as glucose, in body a body fluid such as blood, comprising detecting enhanced electron transfer between an oxidase and a DNA-immobilized electrode, useful for diagnosis of disease -

Example 1; Page 7; 14pp; English.

This invention describes a novel method for quantitatively analysing a biochemical compound (I) which comprises contacting (I) with double translated to the surface of an electrode at their terminals in which electrochemically active threading intercalators are intercalated, in an aqueous medium under application of electric potential to the electrode in the presence of an oxidase which oxidizes the biochemical compound and becomes reduced, and detecting electric current flowing between the electrode and a second electrode in the aqueous medium. The method is useful for detection of biochemical compounds such as glucose, cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic acid in body fluids such as whole blood, plasma, serum, urine, and lymph biochemical compounds quickly and easily with a high sensitivity using a simple apparatus. This sequence represents DNA fragment used as fixed probe DNA in the method of the invention.

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Gaps ., 0 1.5%; Score 17; DB 1; Length 20; .00.0%; Pred. No. 2.1e+02; 0; Indels Best Local Similarity 100. Matches 17; Conservative Query Match

0;

AAA40449 standard; DNA; 20 BP. RESULT 366 AAA40449

·;

Gaps

AAA40449;

13-NOV-2000 (first entry)

Electochemical detection method sample DNA target.

Electrochemical detection; glucose; cholesterol; urea nitrogen; bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood; plasma; serum; urine; lymph diagnosis; ss.

Synthetic.

EP1018646-A2.

12-JUL-2000.

07-JAN-2000; 2000EP-0100126.

99JP-0001111. 99JP-0143599. 06-JAN-1999; 24-MAY-1999;

(FUJF) FUJI PHOTO FILM CO LTD.

Takagi M; Takenaka S, Ogawa M,

WPI; 2000-444372/39.

Quantitative analysis of a biochemical compound such as glucose, in

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This invention describes a novel method for quantitatively analysing a biochemical compound (I) which comprises contacting (I) with double stranded DNA fixed to the surface of an electrode at their terminals in which electrochemically active threading intercalators are intercalated, in an aqueous medium under application of electric potential to the electrode in the presence of an oxidase which oxidizes the biochemical compound and becomes reduced, and detecting electric current flowing between the electrode and a second electrode in the aqueous medium. The method is useful for detection of biochemical compounds such as glucose, cholesterol, urea nitrogen, bilinubin, uric acid, haemoglobin and lactic acid in body fluids such as whole blood, plasma, serum, urine, and lymph for diagnosis of various diseases. The method allows detection of biochemical compounds quickly and easily with a high sensitivity using a simple appearatus. This sequence represents DNA fragment used as a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..19
/*tag= a
/note= "2'-methoxyethoxy modified thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Les
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2'-Methoxyethoxy-modified oligonucleotide.
                                                                                                                                                                                                                                                                                                        sample in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                           Example 1; Page 8; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAAAAAAAAAAAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA50193 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-558188/51.
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA50193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 367
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containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group
on its 5' ribosyl sugar moiety. It is an example of an oligomeric
compound produced according to the methods of the invention. The
invention provides compounds and methods for the preparation of
mixed backbone oligomeric, or chimeric, compounds having
thosphotochioate and/or phosphoramidate internucleoside linkages.
The methods also include incorporation of boranophosphate
internucleoside linkages. The methods utilise H-phosphonate
contiguous region is subsequently oxidized to phosphodiester,
phosphorothioate, phosphoramidate or boranophosphate
internucleoside linkages prior to further elongation. Mixed
backbone oligomeric compounds are prepared in this manner by
oxidizing adjacent regions with different reagents. Oligomeric
compounds of the invention are prepared using novel oxidation steps
that oxidize a region of 1 or more H-phosphonate internucleoside
linkages without degradating existing linkages that have been
previously oxidized. The oligonucleotides obtained are useful as
previously oxidized. The oligonucleotides obtained for other
the previously oxidized. The oligonucleotides obtained are useful as
previously oxidized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stem cell factor universal oligonucleotide 220-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 1; Le
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                research reagents, and as antiviral agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bosselmann RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA13752 standard; DNA; 20 BP.
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90US-0589701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zsebo KM, Suggs SV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-1989;
11-JUN-1990;
24-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA13752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
    body a body fluid such as blood, comprising detecting enhanced electron transfer between an oxidase and a DNA-immobilized electrode, useful for diagnosis of disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of mixed backbone oligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Production of hematopoietic cells suitable for administration to

The present sequence is that of a phosphodiester oligonucleotide

Example 12; Page 34; 49pp; English.

0

Gaps

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subject using progenitor cells and expanding the cells using stem cell

Example 3; Fig 12C; 123pp; English.

administration to a subject. The method comprises: (a) obtaining had administration to a subject. The method comprises: (a) obtaining cadministration to a subject. The method comprises: (a) obtaining to have made the admost of the primary structural specifically by adding to the cells a had admost of the primary structural confirmation and one or more of the blological properties of naturally occurring stem cell factor (SCF). The method is useful for stimulating primitive progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte and macrophage cells. SCF results in absolute increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic progenitors in syngeneic, allogeneic or autologous bone marrow transplant. SCF is useful for enhancing the efficiency of gene therapy based on transfecting haematopoietic stem cells. SCF is also useful for combating the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing the myelosuppressive progenitor acute blood loss and as a boost to the immune system for fighting neoplasia (cancer). The present sequence immune system for fighting neoplasia (cancer). The present sequence the present invention.

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

., Match 1.5%; Score 17; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 2.16+02; es 17; Conservative 0; Mismatches 0; Indels Query Match Matches

1084 AAAAAAAAAAAAA 1100

18 AAAAAAAAAAAAAAAAA

AAA13754 standard; DNA; 20 (first entry) 27-JUL-2000 AAA13754; RESULT 369 AAA13754/C

ВP

Stem cell factor universal oligonucleotide 220-11.

Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia; cancer; ss.

Synthetic.

EP992579-A1

12-APR-2000

90US-0537198. 90US-0573616. 90WO-US05548. 90US-0589701. 99EP-0122861 89US-0422383 04-OCT-1990; 16-0CT-1989 24-AUG-1990 28-SEP-1990 01-OCT-1990

(AMGE-) AMGEN INC.

90EP-0310899

04-OCT-1990;

Suggs SV, Bosselmann RA, Martin FH; Zsebo KM,

deministration to a subject. The method comprises: (a) obtaining has a subject or subject. The method comprises: (a) obtaining the manupoietic progenitor cells from a donor; and (b) expanding the cells did a demantopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally primitive progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte and macrophage cells. SCF results in absolute increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic disorders. The method is useful for expanding early haematopoietic progenitors in syngeneic, allogeneic or autologous bone marrow transplant. SCF is useful for enhancing the efficiency of gene therapy based on transfecting haematopoietic stem cells. SCF is also useful for combating the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing haematopoietic recovery after acute blood loss and as a boost to the immune system for fighting neoplasia (cancer). The present sequence represents a universal oligonucleotide which is used in an example from the present invention. method has been developed of making haematopoietic cells suitable for subject using progenitor cells and expanding the cells using stem cell Production of hematopoietic cells suitable for administration to a Example 3; Fig 12C; 123pp; English. WPI; 2000-259135/23 8XEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE

Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

0

Gaps

Gaps ; 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ative 0; Mismatches 0; Indels 17; Conservative Best Local Similarity Query Match Matches

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1084 AAAAAAAAAAAAAA 1100 N 18 AAAAAAAAAAAAAA Š 셤

AAZ91117 standard; DNA; 20 BP 06-JUN-2000 AAZ91117; RESULT 370 AAZ91117

Oligonucleotide #5 for conjugation to abietane derivative. (first entry)

Abietane derivative; labelling; diagnostic test; biotin substitute; ss.

Synthetic.

FR2781802-A1

04-FEB-2000.

98FR-0010084 31-JUL-1998;

(INMR) BIO MERIEUX.

98FR-0010084

31-JUL-1998;

Delair T, Veron L, Battail PN, Piga N, WPI; 2000-239603/21. Charles MH,

Mandrand

conjugated derivatives with natural and synthetic polymers, having use in diagnostics, chemical reactions and analysis Saturated and unsaturated derivatives of abietic acid and their

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The invention relates to a method for detection of nucleic acid (I) having at least 2 portions, comprising treatment with nanoparticles that
                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide-nanoparticle probe, diagnostic, forensic analysis, nucleic acid detection, nanostructure, biochip; biofilter, drug delivery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and separating nucleic acid, useful e.g. for diagnosis, reaction with nanoparticles that carry oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide-nanoparticle probe #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and separating nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mucic RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementary to parts of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 18; Page 158; 404pp; English
Example 5; Page 20; 39pp; French
                                                                                                                                                                                                                                 1084 AAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                          AAS63428 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2000; 2000US-0603830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-0820279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-200161P.
2000US-213906P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2001; 2001WO-US10071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2000; 2000US-192699P
                                                                                                                                                                                                                                                   20 APAPAPAPAPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Letsinger RL,
Park S, Li Z;
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656926/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Park S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200173123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2000;
26-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mirkin CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting
comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                               AAS63428;
                                                                                                                                                                                                                                                                                     RESULT 371
                                                                                                                                                                                                                                                                                               AAS63428
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carry oligonuclectides complementary to at least 2 parts of (1), where detectable change caused by hybridisation of the oligonuclectide to (1) is observed. The method is used to detect (or to separate) specific (1), e.g. for diagnosing a wide variety of diseases, sequencing, in forensic oligonuclectivatised nanoparticles are also useful for preparing nanostructures useful, for example, as biochips, biofilters, mechanical devices, separation membranes, chemical sensors, in computers, and for drug delivery. Very stable nanoparticle-oligonuclectide conjugates can be produced, allowing their direct use (as probes) in polymerase chain reaction, i.e. they survive multiple heating/cooling cycles so not need to be added after amplification. (1) are detected by simple not med to be added after amplification. (1) are detected by simple repid field testing for e.g. pathogens. Ass63374-AAS63448 represent capid field testing for e.g. pathogens. Ass63374-AAS63448 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
              0;
                                                                          The invention relates to novel saturated and unsaturated abjetane derivatives. The new compounds may be used directly or indirectly in the development of new diagnostic tests, to follow infections, especially viral infections, to follow and/or measure chemical products, especially potential pollutants. In diagnostic tests they may be used as markers, or to form a universal solid phase after immobilization on a solid support, to produce monoclonal antibodies or polyclonal antibodies having diagnostic uses. The oligonucleotides AAS91113-291117 represent examples of sequences that can be labeled with the new abletane derivatives. The new derivatives may be used to substitute for biotin in diagnostic tests, but because they are not found naturally in humans the risk of potential interactions with biological molecules is eliminated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
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Nucleic acid identification; DNA library screening; ss. Nucleotide sequence of a cDNA sequence. 1084 AAAAAAAAAAAAA 1100 AAH78547 standard; cDNA; 20 BP 1 AAAAAAAAAAAAA 17 10-DEC-2001 (first entry) US6274321-B1 Synthetic. AAH78547; RESULT 372 AAH78547 à d

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Gaps

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Length 20; 0; Indels

1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0;

100.0%; Pre

99US-0454704 99US-0454704 (REGC) UNIV CALIFORNIA 03-DEC-1999; 03-DEC-1999; 14-AUG-2001.

Screening nucleic acids (NA) in pool of interest comprises pooling, expressing NA to form expression product pool and identifying NA in NA pool corresponding to expression product pool having interaction with target moiety

WPI; 2001-588900/66.

Blumberg B;

Disclosure; Column 22; 19pp; English.

Storhoff JJ, Elghanian R;

The specification describes a method for identifying a nucleic acid in a pool of interest. The method comprises pooling individually identifiable nucleic acids into at least two pools of one nucleic acid each; expressing nucleic acid pools to obtain protein expression product pools; assaying protein expression product pools for products having interaction with target molecule; selecting nucleic acid pools corresponding to identified protein expression product pools; and identifying individual nucleic acids in identified nucleic acid pools. The method is useful for identifying a nucleic acid (e.g. cDNA) in a pool of interest and for functionally screening several nucleic

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Gaps
acids. The method is also useful for screening genomic DNA libraries or other source of individual CDNAs, mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries. The present sequence
                                                                ·.
                                                 1.5%; Score 17; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
                                                              0; Indels
                                  Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                      Oligonucleotide-cyclic disulphide linker, d.
                                                    100.0%; Prea. ...
                      was used in the course of the invention.
                                                                            1084 AAAAAAAAAAAAA 1100
                                                                                                                             AAS10371 standard; DNA; 20 BP.
                                                                                          1 AAAAAAAAAAAAA 17
                                                                                                                                                        (first entry)
                                                              17; Conservative
                                                       Local Similarity
                                                                                                                                                        24-OCT-2001
                                                                                                                                          AAS10371;
                                                 Query Match
                                                               Matches
                                                                                                                      AAS1037
 8X8888
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Nanoparticle, cyclic disulphide-oligonucleotide, DNA detection, DNA isolation, genetic disease, bacterial disease, viral disease, forensic science, paternity testing, gene therapy, ss. /*tag= a
/note= "A is covalently linked to a
cyclic-disulphide moiety" Location/Qualifiers Key misc_feature Synthetic

WO200151665-A2

19-JUL-2001

12-JAN-2001; 2001WO-US01190.

13-JAN-2000; 2000US-0176409. 26-APR-2000; 2000US-0200161. 26-UUN-2000; 2000US-0603830. 12-JAN-2001; 2001US-0760500.

(NANO-) NANOSPHERE INC.

Letsinger RL, Mucic RC, Storhoff JJ, Elghanian Li Z; Mirkin CA, Taton TA,

WPI; 2001-451868/48.

Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or viral diseases, by contacting the nucleic acid with oligonucleotides attached to nanoparticles and having sequences complementary a portion the nucleic acid

Example 24; Fig 44; 323pp; English

The sequence represents a cyclic disulphide linked oligonucleotide which may be coupled with colloidal gold particles (nanoparticles) and used to demonstrate the method of the invention. The invention relates to isolating or detecting a nucleic acid of interest, in a mixture of nucleic acids, by binding it to 2 or more complimentary nucleotides which have a nanoparticle attached to their 5' ends. The nanoparticles (e.g. colloidal gold) are used to both isolate and detect (e.g. by linking the particle to a fluorescent probe) the resultant complex. The methods are useful for detecting nucleic acids, natural or synthetic, and modified or unmodified. The methods may also be applied in the diagnosis of genetic,

labeling or modifying RNA 3'-termini using DNA polymerase and a synthetic template with defined overhang nucleotides.

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

The sequence represents a synthetic DNA template molecule used to demonstrate the method of the invention. The invention relates to a method of modifying (e.g. 3' end labelling with 32P dAPP) the 3' terminus of an RNA molecule by providing a DNA oligonucleotide, complimentary to the 3' end of the RNA molecule, with an overhang at the 5' end which allows incorporation of the labeling nucleotide into the RNA molecule. The method, based on the synthesis of Okazaki fragments, is useful for labeling and modifying the 3'-termini of other nucleic acids such as DNA fragments. The method is a simple and efficient way of

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0;
bacterial and viral diseases, in forensics, in DNA sequencing, for the ready. The methods are further authentication, and for monitoring gene therapy. The methods are further useful in research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, for quick identification of an infection to assist in drug prescription, and in homes and health centres for inexpensive drug prescription, and in homes and health centres for inexpensive colour change with the methods, which are based on observing colour change with the naked eye, are cheap, fast, simple, robust (reagents are stable), do not require specialised or expensive equipment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying a 3' terminus of a pre-selected DNA sequence, useful for labeling and modifying 3'-termini of other nucleic acids, comprises using a synthetic nucleotide template with a defined overhang nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang;
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                                                                                                                                                                                        1.5%; Score 17; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA template for 3' end labeling of an RNA molecule, #14.
                                                                                                                                                                                                                       Indels
                                                                                                                                                               Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                and little or no instrumentation is required.
                                                                                                                                                                                                      100.0%; Pred. No. 2.1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Column 13; 22pp; English.
                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                      AAS10402 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Szostak JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SZOS/) SZOSTAK J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-366470/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUANG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Gaps

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The present sequence for universal PCR primer 220-3 is 1 of 19
PCR primers (AAS1043-AAS10453) used to amplify various portions of
the human SCF CDNA sequence. The sequence is described in an
invention relating to novel stem cell factors, the polynucleotides
encoding them and methods for producing the stem cell factors. The
methods involve increasing the number of early hematopoietic progenitor
cells in human peripheral blood by administering a haematopoietically
the treatment of blood disorders, including myelofibrosis,
myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,
multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,
Niemann-Pick disease, refractory anaemia, witamin B12 and folic
acid deficiency, hypopigmentation disorders i.e. piebaldism and viral
induced disorders, including AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing the number of early haematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell
                                                                                                                                                                                                                                                                                                Human, stem cell factor; SCF; haematopoietic progenitor cell;
blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
                                                                                                                                                                                                                                                                   Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
      Length 20;
                                     0; Indels
   1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suggs SV, Martin FH;
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                                                                1100
                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0684535.
92US-0982255.
89US-0422383.
90US-0537198.
90US-0573616.
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                                                                1084 AAAAAAAAAAAAAAA
                                                                                              20 AAAAAAAAAAAAAA
                                                                                                                                                                          AAS10447 standard; DNA; 20
                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOSSELMAN R A.
SUGGS S V.
MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            US6248319-B1
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25-NOV-1992;
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01-OCT-1990;
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                                                                                                                                                                                                          AAS10447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZSEB/)
                                                                                                                                             RESULT 375
AAS10447/c
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The present sequence for universal PCR primer 220-11 is 1 of 19 PCR primers (AAS10435-AAS10453) used to amplify various portions of the human SCF CDNA sequence. The sequence is described in an invention relating to novel stem cell factors, the polymucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietically effective human stem cell factor polypeptide. The methods are useful for the treatment of blood disorders, including myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folicacid deficiency, hypopigmentation disorders i.e. piebaldism and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing the number of early haematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell
                                                                                                                                                                                                                                                                            Human, stem cell factor, SCF, haematopoietic progenitor cell;
blood disorder, Hodgkin's disease, vitamin B12, folic acid deficiency;
hypopigmentation disorder, viral disorder, AIDS; PCR primer, ss.
                Gaps
                0;
                                                                                                                                                                                                                                              Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
                Indels
              ..
; Pred. No. 2.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 12C; 210pp; English.
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                                             1084 AAAAAAAAAAAAA 1100
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100.08;
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92US-0982255.
89US-0422383.
90US-0537198.
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90US-0589701.
93US-0172329.
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                                                                           AAAAAAAAAAAAAA
                                                                                                                                                    AAS10449 standard; DNA; 20
                                                                                                                                                                                                                   (first entry)
              17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZSEBO K M.
BOSSELMAN R A
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARTIN F H.
Best Local Similarity
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01-OCT-1990;
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(SUGG/)
(MART/)
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Length 20;

1.5%; Score 17; DB 1; Lv 100.0%; Pred. No. 2.1e+02;

Query Match Best Local Similarity

1.5%; Score 17; DB 1; Length 20;

Query Match

Matches

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RESULT 377

AAH46465/

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20 AAAAAAAAAAAAA 4
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Best Loca Matches

8

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The present invention describes a method for enhancing (E) the efficiency of transfer of a polynucleotide (I) into a target mammalian feal. (II) in vitro, comprising exposing (II) that expresses a stem cell fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (II) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to AAB98190 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                 SCF; stem cell factor receptor; blood cell disorder; primer; mutagenesis; probe; ss.
                                                                                                                                                               Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymucleotide into cell in vitro -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 12C; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 AAAAAAAAAAAAA 1100
                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH41333 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                 93US-0172329.
95US-0449653.
92US-0902593.
92US-091255.
89US-0422383.
90US-0531198.
90US-0531198.
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                                                                                                                                                                                                                                                                                                                                                                 98US-0224681
                                                     AAH41331 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAAAAAAA
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-366062/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                 Stem cell factor;
gene therapy; PCR
                                                                                                                                                                                                                                                                                             US6207454-B1
                                                                                                                                                                                                                                                                                                                                                                 31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1990;
                                                                                                                                                                                                                                                                                                                               27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1993
24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1998
25-NOV-1992
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                                                                                                                             21-AUG-2001
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                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zsebo KM,
                                                                                           AAH41331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                      RESULT 378
                                      AAH41331/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for preparing phosphorothioate oligomorfeotides having at least one nucleoside with a 2' modification. The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid group having at least one nucleoside with a 2' modification in an actonitrile. The present sequence was used to illustrate the method of the present invention. The method is useful for synthesising sulphurised 2' substituted phosphorothioate oligomuclectides, which may be used in molecular biological research, in applications such as anti-viral therapy, and for determining the stereochemical pathways of certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparing sulfurized 2' substituted phosphorothicate oligonucleotides useful in biological research, comprises phosphitylating the 5'-hydroxyl of a nucleic acid having a nucleoside with a 2'
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                          Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note = "All bases are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= "OTHER"
/note= "Modified with 2'-0-methyl"
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheruvallath ZS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy, and for determining the stere enzymes which recognise nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 23; Column 11; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      mod_base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084 AAAAAAAAAAAAA 1100
                                    1084 AAAAAAAAAAAAA 1100
                                                                                                                                                               BP
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                                                                      18 AAAAAAAAAAAAAA
                                                                                                                                                             AAH46465 standard; DNA; 20
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                                                                                                                                                                                                                                    (first entry)
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17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 .20
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                        Oligonucleotide #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-407218/43
                                                                                                                                                                                                                                                                                                                                                                                Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nodified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modification
                                                                                                                                                                                                                                    14-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS6242591-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2001
                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                 AAH46465;
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Best Local S
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0
                            1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ative 0; Mismatches 0; Indels
Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                          AAH41333;
                                                                                                                                                               RESULT 379
AAH41333/c
ID AAH413:
XX
AC AAH413:
XX
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us09904568-1.rng

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PCR primer; ss.
                               Homo sapiens.
                                                           US6207417-B1
                                                                                                                      07-JUN-1995;
                                                                                                                                                                                               24-AUG-1990;
01-OCT-1990;
                                                                                                                                                                  16-OCT-1989;
                                                                                                                                                    21-DEC-1993
                                                                                        27-MAR-2001
                                                                                                                                                                                                                                                                                                                       Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS04113;
                                                                                                                                                                                                                                            ZSEB/)
                                                                                                                                                                                                                                                           BOSS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS04113/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for enhancing (E) the efficiency of transfer of a polynucleotide (I) into a target mammalian facil (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCE) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to AAB98390 represent sequences used in the exemplification
                                                       Stem cell factor; SCF; stem cell factor receptor; blood cell disorder; gene therapy; PCR primer; mutagenesis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide into cell in vitro
                          Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1; Length 20; Pred. No. 2.10+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Bosselman RA, Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 12C; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 AAAAAAAAAAAAA 1100
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98US-0005893.
92US-0982255.
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90US-0537198.
90US-0573616.
90US-0589701.
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                                                                                                                                                                                               98US-0224681.
                                                                                                                                                                                                                             93US-0172329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS04111 standard; DNA; 20
 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-366062/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                    US6207454-B1
                                                                                                                                                                                               31-DEC-1998;
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                                                                                                                                                                                                                             21-DEC-1993;
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24-AUG-1990;
21-AUG-2001
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                                                                                                                                                                  27-MAR-2001
                                                                                                                                                                                                                                                       12-JAN-1998
25-NOV-1992
                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS04111;
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universal oligomucleotides (Asodallo-Asodall) used in the isolation of the human SCF (stem cell factor) cDNA sequence. The present invention relates to novel stem cell factors can be seen invention relates to novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02400 stem cell factors cancoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF (AAU02462-AAU02481) and the oligomucleotides (AAU02462-AAU02481) and the oligomucleotides (AAU02462-AAU02481) and the solation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myelogibrosis, disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, Fulminating septicemia, malaria, vitemin Bl2 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's disease, Kala azar, anaemia and septicemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence for universal PCR primer 220-3 is 1 of 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 12C; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1084 AAAAAAAAAAAAA 1100
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                                                   93US-0172329.
89US-0422383.
90US-0537198.
                                                                                                                                               90US-0573616.
95US-0482918
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Best Local Similarity 100.(
--- hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  piebaldism and vitiligo.
                                                                                                                                                                                                                                      ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-298941/31
                                                                                                                                                                                                                                                                                                   (SUGG/) SUGGS S V. (MART/) MARTIN F H.
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Human, stem cell factor, SCF, early haematopoietic progenitor cell, blood disorder, leukaemia; Hodgkin's disease, lymphoma, splenomegaly, anaemia, Kala azar, septicemia, malaria, hypopigmentation disorder,

Human SCF (stem cell factor) cDNA universal PCR primer 220-3.

AASO4111/(
ID AASO
XX
AC AASO
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DT 29-AI
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Human
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The present sequence for universal PCR primer 220-3 is 1 of 8 universal oligomucleotides (AAS04211-AAS04218) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAU02761-AAU02767, AAU02775, AAU02797) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the oligomucleotides (AAS04182-AAS04210) used in the isolation of human and rat SCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences. The polymicleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, diseeminated fungus disease, Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
              blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early haematopoietic progenitor cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suggs SV, Martin FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 12C; 167pp; English.
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                                                                                                                                                                                                                                                                                92US-0982255.
89US-0422383.
90US-0537198.
90US-0573616.
                                                                                                                                                                                                                                        93US-0172329
                                                                                                                                                                                                                                                                                                                                                                            90US-0589701
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-281051/29.
                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                        PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer; ss.
                                                                                                       Homo sapiens.
                                                                                                                                                 US6218148-B1.
                                                                                                                                                                                                                                        21-DEC-1993;
                                                                                                                                                                                                                                                                                                            16-OCT-1989;
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                                                                                                                                                                                                                                                                                25-NOV-1992;
                                                                                                                                                                                                                                                                                                                             11-JUN-1990;
24-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1990;
                                                                                                                                                                                            17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS04214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS04214/c
                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence for universal PCR primer 220-11 is 1 of 8
universal oligonucleotides (AASO4110-AASO4117) used in the
isolation of the human SCF stem cell factor. DNA sequence. The
present invention relates to novel stem cell factors

(AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
cncoding them. SCF stimulate primitive progenitor cells including early
haematopoletic progenitor cells. The invention also describes SCF
peptides (AAV02462-AAV07481) and the oligonucleotides

(AASO4081-AASO4117) used in the isolation of human and rat SCF
sequences. The polynucleotide encoding SCF is useful for producing
caute leukaemia, multiple myeloma, Hodgkin's disease, lumphoma,
acute leukaemia, multiple myeloma, Hodgkin's disease, lumphoma,
daucher's disease, anaemia, congestive splenomegaly, Kala azar,
Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
Caucher's military tuberculosis, disseminated fungus disease,
Fulminating septicemia, malaria, vitemin B12 and folic acid deficiency,
pyridoxine deficiency, and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's disease, Kala azar, anaemia and septicemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; stem cell factor; SCF; early haematopoietic progenitor cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 1; Le
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 12C; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.5%; Soc
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                89US-0422383.
90US-0537198.
90US-0573616.
90US-0589701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      piebaldism and vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                          ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-298941/31.
                                                                                                                                                                                                                                                                              16-OCT-1989;
11-JUN-1990;
24-AUG-1990;
                                                                                  Homo sapiens
                                                                                                                          JS6207417-B1
                                                                                                                                                                                                                 37-JUN-1995;
                                                                                                                                                                                                                                                         21-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                  01-OCT-1990;
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                                                                                                                                                                      27-MAR-2001
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Gaps

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US6204363-B1

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The present sequence for universal PCR primer 220-11 is 1 of 8 universal oligomucleotides (AAS04218) used in the isolation of the human SCF (stem cell factor) cDNA sequence. The present invention relates to novel stem cell factors

(AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides cancoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF (ARS04182-AAS04210) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metabetatic carcinoma, acute leukaemia, multiple myeloma, Hoddytin's disease, lymphoma, gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sanchosis, military tuberculosis, disseminated fungus disease, ruliminating septicemia, malazia, vitamin B12 and folic acid deficiency, signal and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                 Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early haematopoietic progenitor cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 17; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 12C; 167pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH23889 standard; DNA; 20 BP
                                                                                                                                                              89US-0422383.
90US-0537198.
90US-0573616.
90US-0589701.
                                                                                                                93US-0172329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100. Les 17; Conservative
                                                                                                                                                                                                                                                                                   Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       piebaldism and vitiligo.
                                                                                                                                                                                                                                                                                                                   WPI; 2001-281051/29
                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                 Homo sapiens.
                                               US6218148-B1
                                                                                                                21-DEC-1993;
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                                                                               17-APR-2001
                                                                                                                                                25-NOV-1992
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                                                                                                                                                                               11-JUN-1990
                                                                                                                                                                                                 24-AUG-1990
                                                                                                                                                                                                                                                                                  Zsebo KM,
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Matches
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acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcindosis, military tuberculosis, disseminated fungus disease, Fulminating septicaemia, malaria, vitamin BL2 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                  New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence for universal PCR primer 220-3 is 1 of 8 universal oligonucleotides (AAH23888-AAH23895) used in the isolation of the human SCF (Stem cell factor) cDNA sequence. The present invention relates to novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including especial progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides (AAB73578-AAB73597) and the oligonucleotides (AAB7389-AAB73897) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing family useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                              Zsebo KM, Bosselman RA, Suggs SV, Martin FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 12C; 166pp; English.
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                                                                                                 91US-0684535.
89US-0422383.
90US-0537198.
90US-0573616.
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                                                                    92US-0982255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                piebaldism and vitiligo.
                                                                                                                                                                                                                                                                               WPI; 2001-256683/26.
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Best Local Similarity
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                                                                                                                  16-OCT-1989;
11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
                                                                    25-NOV-1992;
                                 20-MAR-2001
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Matches
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Gaps

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PCR primer; ss.

PCR primer; ss. Homo sapiens.

Homo sapiens. US6204363-B1 05-APR-2001

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universal oligonucleotides (AAH23895) used in the isolation of the human SCF (stem cell factor) CDNs sequence. The present invention relates to novel stem cell factor) CDNs sequence. The present invention relates to novel stem cell factors (AAB73561, AAB73576) and the polynucleotides (AAB73561, AAB73577). AAB73577 and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early hamatopoletic progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides (AAH23897) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, cut leukamia, multiple myeloma, disease, lymphoma, daucher's disease, anaemia, congestive splenomegally, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, printinating septiceamia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                            New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence for universal PCR primer 220-11 is 1 of 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 1; Length 20;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                           Suggs SV, Martin FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 12C; 166pp; English.
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90US-0537198.
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90US-0589701.
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                                                 92US-0982255.
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                                                                                                                                                                                                                           Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                             WPI; 2001-256683/26.
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                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200122972-A2.
                                                                                                                                                                                        (AMGE-) AMGEN
                                                 25-NOV-1992;
                                                                                                   16-OCT-1989;
11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-2001
                                                                                   10-APR-1991;
                                                                                                                                     24-AUG-1990;
01-OCT-1990;
                20-MAR-2001
                                                                                                                                                                                                                          Zsebo KM,
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-parasitic;
                                                                                                                                                                                                                                                    Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-par
immunostimulatory, tumour; viral infection, bacterial infection,
fungal infection, parasitic infection, cancer, asthma,
infectious disease, allergy, immune deficiency, phosphorothicate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: the present sequence may have a phosphorothioate backbone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid #543.
                                                                                                                                                                                                                                                                                                      Claim 101; Page 42; 338pp; English.
                                                                                                                                                                                   Schetter C, Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
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27-SEP-1999; 99US-0156135.
23-AUG-2000; 2000US-0227436.
                                                                               27-SEP-1999; 99US-0156135
23-AUG-2000; 2000US-0227436
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                               25-SEP-2000; 2000WO-US26383
                                                                 99US-0156113
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                                                                                                                                 (IOWA ) UNIV IOWA RES FOI
(COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                    WPI; 2001-273485/28
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                                                                 25-SEP-1999;
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                                                                                                                                                                                   Krieg AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Krieg AM,

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (r) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, hemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a fine to a Thl immune response and to activate immune cells.

Note: the present sequence may have a phosphorothioate backbone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; membrane; cytostatic; virucide; vasotropic; dermatological; antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense; tumor therapy; drug; phosphodiester linkage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New substituted aryl conjugates of parent molecules, especially oligonucleotides, having improved transmembrane and intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport properties, useful as medicaments or diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; Partive 0; Mismatches 0; Indels
  using immunostimulatory Py-rich and TG nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugate forming oligonuclectide ON5 SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gothe G,
                                                       Claim 101; Page 49; 338pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS PHARMA DEUT GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greiner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-203679/21.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF60896;
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                                                                                                                                                                                                                                                                                                             The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxcoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection, bacterial infection; fungal infection; parasitic infection; cancer, asthms; infectious disease; allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                     Vaccinating against tumors, infectious diseases, allergies and asthma
using immunostimulatory Py-rich and TG nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: the present sequence may have a phosphorothicate backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.5%; Score 17; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunostimulatory nucleic acid #547.
                                                                                                                                                                                                                                                                   Claim 101; Page 49; 338pp; English
                                                                              Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vollmer J;
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27-SEP-1999; 99US-0156135.
23-AUG-2000; 2000US-0227436.
(IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
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(COLE-) COLEY PHARM GMBH
                                                                              Schetter C,
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Schwerdel M;

Synthetic

AAF99431;

RESULT 388 AAF99431

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Krieg AM,

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Gaps

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Length 20;

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the directly or via a chemical group, provided that the chemical group is other than CH 2-S if the bond is via a phosphodiester linkage of (A). The invention also describes (i) the preparation of a conjugate (I') of (A') a molecule to be transported and (B') at least one aryl residue (not creatized to (II)), by preparing (A') containing a reactive function at the position at which (B') is to be bonded, preparing (B') and reacting (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded (C') at a chemical group) for transporting (A) across biological membranes. The products of the invention have cytostatic, virucide, vasorropic, corresponding of the invention have cytostatic, virucide, vasorropic, corresponding of the invention have cytostatic, virucide, vasorropic, corresponding (A) across biological membranes or into eukaryotic or prokaryotic cells (A) across biological membranes or into eukaryotic or prokaryotic cells (A) across biological membranes or into eukaryotic or prokaryotic cells, containing (I) are also claimed. Typically (I) are also claimed. Typically (I) are also claimed. Typically (I) are antisense or into the transporting or cells. Medicaments, diagnostic agents and test kits containing (I) are also claimed. Typically (I) are antisense or inference for tunor therapy, oligonucleotide drivatives for transing viral infections or diseases associated with integrins or cellicallization. Conjugates for in vivo diagnostic use, e.g. by in situ or hybridization. Conjugates for in vivo diagnostic use, e.g. by in situ collications or diseases associated with integrins or cellular uptake etc. The capital are uptake etc. The capital of cellular uptake conjugated with fluorescein derivative residues, cellular uptake to corresponding fluorescein centurated (II); e.g. oligonucleotides conjugated with fluorescein derivative to that obtained using other conjugated vith fluorescein derivative r conjugates.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

. 0 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels 17; Conservative Similarity Query Match Local Matches

1084 AAAAAAAAAAAAA 1100 AAAAAAAAAAAAA 17

> Š g

AAF28351 standard; DNA; 20 RESULT 390 AAF2835

AAF28351;

BP

02-APR-2001

(first entry)

DNA oligomer #1.

Deoxymucleic S-Methythiourea; DNmt; antisense therapy; cardivovascular disease; inflammatory disease; neurocellular disease; antiviral therapy; human immunodeficiency virus; human-cytomegalovirus; influenza; herpes; infection; se.

JS6169176-B1

12-JAN-2001

99US-0407675. 32-JUL-1998; 28-SEP-1999;

98US-0091481. 98US-0111800. 99US-0347443. 11-DEC-1998; 02-JUL-1999;

REGC) UNIV CALIFORNIA.

Dev AP,

WPI; 2001-122276/13.

Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in

The present sequence was used to demonstrate the ability of decxynucleic S-Methythiourea (DNMt) compounds to form triplexes with DNA oligomers. An increase in the C content of the oligos realized in a large decrease in binding. This experiment was performed as an example of a method for preparing oligomucleotides comprising a backbone of alkyl or alkoxy thiourea linkages. The method is useful for preparing oligomucleotides for use in antisense or antigene therapy, to inhibit production of proteins associated with genetic diseases, cardiovascular, inflammatory and neurocellular diseases, and for antivirus therapy, e.g. to treat human immunodeficiency virus, human-cytomegalovirus, influenza and to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind and by antagonising the normal biological cuissue e.g. tissue differentiation, both in vivo and in ex vivo tissue cultures. The method provides an efficient and rapid solid-phase method for the synthesis of thiourea and S-methylthiourea. 0 by synthesizing oligonuclectides comprising backbone thiourea linkages in solution or on solid phase -Gaps 0; 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; 0; Indels Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; Query Match Best Local Similarity 100.0%; Pred. No. 2... Matches 17; Conservative 0; Mismatches Example 7; Fig 16; 48pp; English. 1084 AAAAAAAAAAAAAA 1100 antisense therapy, of alkyl or alkoxy

1 AAAAAAAAAAAAAA 17 à g

RESULT 391 AAF28481

.; 0

Gaps

AAF28481 standard; DNA; 20 BP.

AAF28481;

03-APR-2001 (first entry)

Random oligonucleotide, SEQ ID NO: 53.

Nucleic acid detection, nanoparticle-oligonucleotide conjugate, digease diagnosis, forensic analysis, DNA sequencing, paternity testing; disease diagnosis; torensic analyses, correctl line authentication; gene therapy; ss.

Synthetic.

WO200100876-A1.

04-JAN-2001.

26-JUN-2000; 2000WO-US17507.

25-JUN-1999; 99US-0344667. 26-APR-2000; 2000US-0200161. MIRKIN C A.
LETSINGER R L.
MUCIC R C.
STORHOFF J J. (MIRK/)

ELGHANIAN R. (LETS/)
(MUCI/)
(STOR/)
(ELGH/)
(TATO/)

TATON T A.

Storhoff JJ, Elghanian R; Mirkin CA, Letsinger RL, Mucic RC, Taton TA;

WPI; 2001-061976/07

Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics and DNA sequencing, comprises observing detectable change

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The present sequence is an oligonuclectide used in a method for detecting a nucleic acid having at least 2 portions. The method comprises hybridising the nucleic acid with oligonuclectides, such as the present sequence, attached to a substrate and/or particle and detecting a change in colour, conductivity or optical density. The method is useful for the diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing, for paternity testing, for cell line authentication and for monitoring gene therapy. Detecting nucleic acids based upon observing a colour change is cheap, fast, simple, and does not require specialised or expensive equipment. The nanoparticle oligonucleotide conjugates remain stable for at least 6 months. A single base mismatch and as little as 20 femtomoles (fM) of target can be detected using the conjugates.
brought about by hybridization of nucleic acid with substrate or particle bound oligonucleotides -
                                                                                    Disclosure; Page 199; 205pp; English.
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Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Gaps 0; Length 20; 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; Ative 0; Mismatches 0; Indels 17; Conservative Query Match Best Local Similarity Matches

0;

셤

RESULT 392

AAC87230 standard; DNA; 20 AAC87230/c CCCCX SX X B X B X X B X

BP

AAC87230;

(first entry) 09-MAR-2001

Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.

Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN; 'mmunoerimulatory DNA-binding protein; nucleolin; hnRNP D; AUFl; immunostimulatory DNA-binding protein; nucleolin; hnRNP Ď, AUF1. hnRNP A1; lupus La protein; functional modificar identification; agonist; antagonist; mimic; inhibitor; drug screening; cellular target identification; oligonucleotide optimisation; immunotherapy; ss.

Synthetic

WO200067023-A1

09-NOV-2000.

28-APR-2000; 2000WO-US11697

99US-0131830 03-MAR-2000; 2000US-0186845 29-APR-1999;

(CPGI-) CPG IMMUNOPHARMACEUTICALS (IOWA) UNIV IOWA RES FOUND.

GMBH.

Krieg AM; Schetter C, Noll BO,

WPI; 2001-016002/02

Immunostimulatory DNA binding proteins to identify immunostimulatory DNA functional modifiers, immunostimulatory DNA binding competitors to optimize immunostimulatory oligodeoxynucleotides for stimulation

Example 1; Page 45; 95pp; English.

The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to it and thereby act as functional modifiers of immunostimulatory

Consist of immunostimulatory DNA agonists and antagonists.

DNA mimics, and immunostimulatory DNA agonists and antagonists.

Immunostimulatory DNA-binding inhibitors, immunostimulatory DNA-binding proteins can also be used in remostimulatory DNA-binding proteins can also be used in membrace in immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA-binding protein bound to an immunostimulatory DNA binding protein bound to candidate carget molecules to identify the cellular target molecules of the immunostimulatory DNA-binding proteins used in the methods of the invention are the RNA-binding proteins nucleolin, hnRNP D, ADPI, hnRNP AI and lupus La protein. The screening methods are useful for identifying a compound that inhibits interaction between immunostimulatory DNA and an immunostimulatory DNA cellular target complex is useful in screening for immunostimulatory DNA cellular target molecules. The candidate immunostimulatory DNA cellular target molecules. The candidate immunostimulatory ODNS competitors allow the investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The present sequence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The present sequence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The presents equence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The presents sequence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The presents sequence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The presents sequence investing immunostimulatory DNA-binding proteins and immunostimulatory ODNS. The present sequence investing in the pr .. Gaps Such modifiers of ODN activity . 0 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; 0; Indels Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other; 100.0%; Preq. ... oligodeoxynucleotide (ODN) activity. 1084 AAAAAAAAAAAAA 1100 20 AAAAAAAAAAAAAA 4 Best Local Similarity 100. Matches 17; Conservative invention. Query Match ð a

RESULT 393 AAC87238/

AAC87238 standard; DNA; 20 BP. AAC87238;

09-MAR-2001 (first entry)

Phosphorothicate poly T oligonuclectide, SEQ ID NO:17.

Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN, immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1; hnRNP A1; lupus La protein; functional modificar identification; agonist; antagonist; mimic; inhibitor; drug screening; cellular target identification; oligonucleotide optimisation; immunotherapy; ss

Synthetic

WO200067023-A1.

09-NOV-2000

28-APR-2000; 2000WO-US11697. 29-APR-1999; 99US-0131830. 03-MAR-2000; 2000US-0186845.

CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH (IOWA) UNIV IOWA RES FOUND

Krieg AM; Schetter C, Noll BO,

WPI; 2001-016002/02.

Immunostimulatory DNA binding proteins to identify immunostimulatory DNA functional modifiers, immunostimulatory DNA binding competitors and to optimize immunostimulatory oligodeoxynucleotides for stimulation -

Example 1; Page 45; 95pp; English.

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consist of immunostimulatory DNA binding inhibitors, immunostimulatory Consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA binding inhibitors, immunostimulatory DNA binding inhibitors, immunostimulatory DNA agonists and antagonists.

DNA minics, and immunostimulatory DNA agonists and antagonists.

Concerning methods to identify immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding protein bound to an immunostimulatory ON can additionally be used to screen a panel of candidate target molecules to identify the cellular target molecules of the immunostimulatory DNA-binding proteins used in the methods of the invention are the RNA-binding proteins nucleolin, hnRNP D, AUFI, hnRNP A1 and lupus La protein. The screening methods are useful for identifying a compound that inhibits interaction between immunostimulatory DNA and an immunostimulatory DNA-binding protein and for identifying agonists useful in immunocharapy. The complex is useful in screening methods is useful in screening for immunostimulatory DNA-binding complex is useful in screening methods is useful in screening methods in methods are useful for identifying agonists useful in immunocharapy. The complex is useful in screening methods are useful for identifying of immunostimulatory DNA-binding complex is useful in screening methods.
                      The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to it and thereby act as functional modifiers of immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecules. The candidate immunostimulatory ODN competitors allow the investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory ODNs. The present sequence represents an oligonucleotide used in an exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 1; Le
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly T oligonucleotide, SEQ ID NO:20.
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Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nvention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC87241;
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X2555555555555555555555555555555
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The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to it and thereby act as functional modifiers of immunostimulatory oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity. Such modifiers of ODN activity consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA agonists and artagonists. Immunostimulatory DNA agonists and artagonists. Immunostimulatory DNA-binding proteins can also be used in screening methods to identify immunostimulatory DNA binding protein competed and to optimize an immunostimulatory ODN for immune stimulation. Isolated complexes of an immunostimulatory DNA-binding protein bound to an immunostimulatory ODN for immunostimulatory ODN can additionally be used to screen a panel of candidate target molecules to identify the cellular target molecules of the invention are the RNA-binding proteins used in the methods of the invention are the RNA-binding proteins methods are useful for identifying a compound that inhibits interaction methods are useful for identifying a compound that inhibits interaction protein and for identifying agonists useful in immunostimulatory DNA and immunostimulatory DNA binding protein and for identifying agonists useful in immunostimulatory DNA cellular target complex is useful in screening for immunostimulatory DNA cellular target increasing in the immunostimulatory DNA collular target increasing the immunostimulatory DNA by complex is useful in screening for immunostimulatory DNA cellular target increasing the immunostimulatory DNA cellular target increasing the immunostimulatory DNA by complex is useful in screening for immunostimulatory DNA cellular target increasing the immunostimulatory DNA by immunostimulatory DNA cellular target increasing the immunostimulatory DNA cellular target inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory ODNs. The present sequence represents an oligonucleotide used in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
DNA functional modifiers, immunostimulatory DNA binding competitors to optimize immunostimulatory oligodeoxynucleotides for stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian stem cell factor PCR primer SEQ ID NO: 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                            Example 1; Page 45; 95pp; English.
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Best Local Similarity 100.0
Matches 17; Conservative
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11-JUN-1990;
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Gaps

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Length 20; 0; Indels Martin FH;

Suggs SV,

Bosselman RA,

Zsebo KW.

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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFs). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial garm stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention.
                                        Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early haematopoietic progenitor cells, useful for treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic aneemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID;
                                                                                                                                                                                                                                                                                                                        / Match 1.5%; Score 17; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 2.1e+02; les 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    severe combined immunodeficiency; PCR primer; ss
                                                                                                                                                                                                                                                                                               Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                  Example 3; Fig 12C; 209pp; English.
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89US-0422383.
90US-0537198.
90US-0573616.
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                                                                                    Barcoidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 396
                                                                                                                                                                                                                                                                                                                                                       Matches
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Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early haematopoietic progenitor cells, useful for treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,

Example 3; Fig 12C; 209pp; English

sarcoidosis

Suggs SV, Martin FH;

Bosselman RA,

Zsebo KM,

WPI; 2001-353108/37.

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Gaps

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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFS). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglobinuxia, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to an array of proteins (antibody minics) comprising a fibronectin type III domain having a randomised loop, a bind tearsheet, or their combination, and has the capacity to bind to a compound that is not bound by a corresponding naturally-occurring fibronectin, immobilised onto a solid support. The antibody mimics is useful for detecting a compound preferably a protein, in a biological sample. It is also useful to detect one or more different analytes simultaneously in a sample. Hence is useful for diagnostic purposes. It is also useful for the purpose of designing proteins capable of binding to virtually any compound of interest. The present sequence is a capture probe used to self-assemble and anchor the tenth module of human fibronectin module of type III (Fn3) (10Fn3) which is used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibronectin scaffold protein array for obtaining a protein/compound which binds to a compound/protein, comprises a fibronectin type III domain having a randomized loop, a randomized beta-sheet or their
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scaffold protein; antibody mimic; fibronectin type III domain; randomised loop; randomised beca-sheet; diagnostic purpose; protein designing; probe; tenth module of human Fn3; 10Fn3; fibronectin module of type III; Fn3; ss.
                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                              ch 1.5%; Score 17; DB 1; Le 1. Similarity 100.0%; Pred. No. 2.1e+02; 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                         Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD16997 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-557782/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capture probe CP5'.
                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD16997;
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD16997,
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SCF universal oligonucleotide 220-11.
                                                                                                                                                                                                                                                                                                                     Bosselman RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                  89US-0422383.
90US-0537198.
90US-0573616.
90WO-US05548.
90US-0589701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                   90EP-0310899.
                                                                                                                                                           2002EP-0008587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 АААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS73850 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  haematopoietic system;
                                                                                                                                                                                                                                                                                                                                                                                                             the human SCF
                                                                                                                                                                                                                                                                                                                     Suggs SV,
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-684093/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                           04-OCT-1990;
                                                                                                        EP1241258-A2
                                                                                                                                                                                                 1990;
                                                                                                                                                                                                                                                   04-OCT-1990;
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01-OCT-1990;
                                                                                                                                 18-SEP-2002.
                                                                                                                                                                                    16-0CT-1989,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-2002
                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                     Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                             encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS73850;
                                                                                                                                                                                                11-JUN-1
24-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS73850/
ID ABS77
AC ABS77
XX ABS77
XX CS-D
XX CS-D
XX SCE
XW Stem
XW Stem
XW Maem
XW mult
XW mult
XW refr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carrying out a thermal cycle of polymerase chain reaction (PCR) by using a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stem cell factor; SCF; blood-forming system; blood cell disorder;
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0
                       1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         reaction; thermal cycle; immobilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
                                                                                                                                                                                                                                                Nucleotide seguence of a PCR primer #1
                                                                                                                                                                                                                                                                                    genetic engineering; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCE universal oligonucleotide 220-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Page 9; 13pp; Japanese.
                                                                           1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAA 1100
                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2000; 2000JP-0399573
                                                                                                                                                          871/c
ABQ79871 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-2000; 2000JP-0399573
                                                                                                     20 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS73848 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAAAAAAAAAAA
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (TOJO ) TOYO KOHAN CO LID.
(TAKA/) TAKAHASHI K.
                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-630904/68.
                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                          chain
                                                                                                                                                                                                                                                                                                                                          JP2002191369-A
                                                                                                                                                                                                                       23-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002
                                                                                                                                                                                                                                                                          Polymerase
                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                             ABQ79871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                        Query Match
                                                  Matches
                                                                                                                                            RESULT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 399
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                                                                                                                                                       ABQ79871/
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Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukaemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA
multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antianaemic; antifungal; antimalarial; dermatological; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorlectide sequences encoding the SCFS, and methods of producing them. SCFs are involved in the blood-forming (haematopoietic) superior are involved in the blood-forming (haematopoietic) is useful for the production of humans. The method of the invention is useful for treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemai, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present used in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stem cell factor; SCF; blood-forming system; blood cell disorder; haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
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14-DEC-2001; 2001WO-US48458.
                                                                                                                                              Bratzler RL;
                                                   11-JUL-2002
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    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS78072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS78072/
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                 Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukaemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA encoding the human SCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; telangiectasia; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel stem cell factors (SCFS), polymucleotide sequences encoding the SCF6, and methods of producing them. SCF8 are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence representing a universal oligonucleotide for SCF DNA is used in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
antianaemic; antifungal; antimalarial; dermatological; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Bosselman RA, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiogenesis inhibitory oligonucleotide #226.
                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 12C; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 AAAAAAAAAAAAA 1100
                                                                                                               89US-0422383.
90US-0537198.
90WG-0573616.
90WG-U505548.
90US-0589701.
95EP-0105391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABS77742 standard; DNA; 20 BP
                                                                                           2002EP-0008587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                    Suggs SV,
                                                                                                                                                                                                                                                          WPI; 2002-684093/74.
                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                           04-OCT-1990;
                                                                                                                                                  28-SEP-1990;
01-OCT-1990;
04-OCT-1990;
                                             EP1241258-A2
                                                                                                                                                                                       04-OCT-1990;
                                                                                                                            11-JUN-1990;
24-AUG-1990;
                                                                   18-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-2002
                       Synthetic
                                                                                                                                                                                                                                    Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS77742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule.

Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis.

The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthitis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, intestinal adhesions, atheroselerosis, scleroderma and hypertrophic scars. The present structure is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophilac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 1.5%; Score 17; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 2.1e+02;
les 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitory oligonucleotide #556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 23; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084 AAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                     PHARM GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS78072 standard; DNA; 20 BP.
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                                                                                                                                                        14-DEC-2001; 2001WO-US48458
                                                                                                                                                                                                                                   14-DEC-2000; 2000US-255534P.
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WO200253141-A2.
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COLE-) COLEY PHARM GROUP INC.
                                                                                                                                                                                                       14-DEC-2000; 2000US-255534P.
                                                                                                                                                                                                 14-DEC-2001; 2001WO-US48458
                    WPI; 2002-566690/60.
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                     WO200253141-A2.
                                                                                                                                        13-DEC-2002
                                                                                                                                                                                           11-JUL-2002
                                                                                                                                                                                                                   Bratzler RL;
                                                                                                                                   ABS78076;
                                                                                                                      RESULT 403
                                                                                                 Matches
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic uncluded is a kit comprising a first container housing them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolantal fibroplasia, rubeosis, Osler Webber Syndrome, mycoardial angiogenesis, plaque neovascularisation, intestinal adhesions, mangiofibroma, wound granulation, intestinal adhesions, angiofibroma, wound granulation, intestinal adhesions, atheroselerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid detection method, nanoparticle-oligonucleotide conjugate, nanoparticle, viral RNA detection, bacterial DNA detection; fungal DNA detection;
                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid detection method associated polynucleotide #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.5%; Score 17; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                    Claim 2; Page 29; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS64673 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000US-25418P.
11-DEC-2000; 2000US-255235P.
11-DEC-2000; 2000US-255236P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-080279;
09-APR-2001; 2001US-282640P.
10-AUG-2001; 2001US-0927777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-2001; 2001WO-US46418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-254392P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NANO-) NANOSPHERE INC.
WPI; 2002-566690/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200246472-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS64673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS64673
ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                           The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antianglogenic nucleic acid molecule.

Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering the antianglogenic nucleic acids, and instructions for administering them to as subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial joints, angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiotibroma, wound garanulation, intestinal adhesions, seleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                     comprising
                                                                                                                                                                                              Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriaais; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                      The invention relates to inhibiting angiogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                        Claim 2; Page 29; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 AAAAAAAAAAAAA 1100
                                                     (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABS78076 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AAAAAAAAAAAAAA 4
       14-DEC-2000; 2000US-255534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Gaps · 0

Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and

Storhoff JJ, Elghanian R;

Letsinger RL, Mucic RC, St Garimella V, Li Z, Park S;

Mirkin CA,

Taton TA,

WPI; 2002-608256/65.

Page 181

The invention describes a method of detecting (MI) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides to two portions involving providing nanoparticles having oligonucleotides portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (MI), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or portions, such as viral RNA, bacterial or fungal DNA, a gene associated more nucleic acids (Irom a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification.

(II) is useful for preparing a nucleic acid bound to an electrode surface. In and (II) are useful for fabrication, and for separating a selected nucleic acid having two portions from other nucleic acide (I), (II) and polymerate probe are useful for detecting an analyte (especially polymerate) in a sample of the aggregate probe are useful for detecting an analyte (especially bolymerate) in a sample. nanoparticles to allow hybridization, and observing detectable change polyvalent analyte) in a sample. This sequence represents a polynuclectide used to demonstrate the method of the invention. Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; Example 18; Page 437; 442pp; English

1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 17; Conservative

ö

Gaps

; 0

1084 AAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAA 17 à

ABS64688 standard; DNA; 20 BP ABS64688; RESULT 405 ABS64688

(first entry) 15-NOV-2002

Nucleic acid detection method associated polynucleotide #70.

Nucleic acid detection method, nanoparticle-oligonucleotide conjugate, nanoparticle, viral RNA detection; bacterial DNA detection; fungal DNA detection;

Synthetic

WO200246472-A2.

13-JUN-2002

07-DEC-2001; 2001WO-US46418.

08-DEC-2000; 2000US-254392P.
08-DEC-2000; 2000US-254418P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-255236P.
28-MAR-2001; 2001US-076550.

(NANO-) NANOSPHERE INC

10-AUG-2001;

Storhoff JJ, Elghanian R; Letsinger RL, Mucic RC, SI Garimella V, Li Z, Park S; Mirkin CA, Taton TA,

WPI; 2002-608256/65.

The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonuclectides attached to it, which has a sequence complementary to sequence of two portions of mucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonuclectides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (M1), nanoparticles (I), nanoparticle-oligonuclectide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. (II) and (II) are useful for fabrication, and for separating a selected nucleic acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (sepecially conjugate) in a sample. This sequence represents a 0; Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change Gaps polyvalent analyte) in a sample. This sequence represents a polynuclectide used to demonstrate the method of the invention. .; Nuery Match 1.5%; Score 17; DB 1; Length 20; Jest Local Similarity 100.0%; Pred. No. 2.1e+02; Atches 17; Conservative 0; Mismatches 0; Indels Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; Example 24; Fig 44; 442pp; English. 1084 AAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAA 17 Query Match

ð qq

ABN87103/c ID ABN87103 standard; DNA; 20 ABN87103; RESULT 406

30-JUL-2002 (first entry)

Capture probe CP5' SEQ ID NO:23.

Protein scaffold, antibody, binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.

Synthetic

WO200232925-A2.

25-APR-2002

16-OCT-2001; 2001WO-US32233.

16-OCT-2000; 2000US-0688566.

(PHYL-) PHYLOS INC.

Kuimelis RG Lipovsek D, Wagner RW,

WPI; 2002-444238/47

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest

us09904568-1.rng

Disclosure; Page 58; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference domain having an immunoglobulin-like fold, derived from a reference protein baving a mutated amino acid sequence, where the non-antibody is protein binds with a Kd at least as tight as 10 mM to a compound that is protein is useful as scaffolds for selecting or designing a protein or framework with specific and favourable properties, e.g. for binding any antiped of interest, or for destroying or inactivating antibody antibodies are used, e.g. research, therapeutic or diagnostic fields, antibodies are used, e.g. research, therapeutic or diagnostic fields, antibodies are used, e.g. research, therapeutic or diagnostic fields, antibodies are used, e.g. research, therapeutic or diagnostic fields, cantibodies are used, e.g. research, therapeutic or diagnostic fields, antibodies are used, e.g. research, therapeutic or diagnostic fields, chose of natural antibodies, and can be evolved rapidly in vitro. The properties, such as stability under reducing conditions and solubility properties, such as stability under reducing conditions and solubility experties, such as stability under reducing conditions and solubility expressed and folded in prokaryotic systems (e.g. Bacherichia coli), in expressed and folded in prokaryotic systems (e.g. Bacherichia coli), in are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein extremely contended in the exemplification of the present invention.

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

ö Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

1084 AAAAAAAAAAAAAA 1100

Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelosciprosis; osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; bi quojielmo syndrome; congestive splenomegaly; splenic pancytopaenia; diseaminated fungus disease; Fulminating septicaemia; piebaldism; AIDS; acquired immune deficiency syndrome; malaria; miltary tuberculosis; pyridoxine deficiency syndrome; malaria; miltary tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; blamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR; primer;

Rattus sp

US2002018763-A1.

g

AAD35464 standard; DNA; 20 BP. 25-JUL-2002 (first entry) AAD35464; RESULT 407

Rat SCF 5' cDNA amplifying PCR primer, 220-3.

14-FEB-2002.

98US-0005243. 95US-0449653 12-JAN-1998; 24-MAY-1995;

(ZSEB/) ZSEBO K M. (BOSS/) BOSSELMAN R A. (SUGG/) SUGGS S V.

Bosselman RA, (MART/) MARTIN F H Zsebo KM,

Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal Suggs SV, Martin FH; WPI; 2002-350789/38

Example 3; Fig 12C; 217pp; English.

The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, aneemia and for enhancing bone marrow accovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemocharapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal camage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypenitor cells with a gene, and transfection of early costeopetrosis, metastatic carcinoma, acute leuksemia, multiple myeloma, costeopetrosis, disease, lamphoma, Gaucher's disease, Niemann-Pick disease, nedgrin, disease, refractory erythroblastic anaemia, Dickinsty cospience pancytopaenia, diseaminated fungus disease, malaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin cost disorders such as piebaldism, AIDS (acquired immune deficiency, vitamin and titiligo. The present sequence is a PCR primer which is used for amplification of rat SCF CDNA. This sequence is used in the exemplification of the invention.

Seguence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

0; Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

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AAD35466 standard; DNA; 20 BP. AAD35466; RESULT 408 AAD35466/

25-JUL-2002 (first entry)

Rat SCF 5' cDNA amplifying PCR primer, 220-11.

Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelosolerosis; osteopetrosis; metastatic carctinoma; acute leuksemia; multiple myeloma; sarcoidosis; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; Di Guglielmo syndrome; congestive splenomegaly; splenic pancycopaenia; diseaminated fungus disease; Fulminating septicaemia; piebaldism; ADEs, pyridoxine deficiency; syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;

Rattus sp

WO200218643-A2.

Synthetic.

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The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently chartor (SCF) polypeptides having an amino acid sequence sufficiently countring SCF to allow possession of duplicative of that of naturally-occurring SCF to allow possession of anomatopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopeania, thrombocytopeania, anaemia and for enhancing bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerved damage, neoplasia, infertility, myeloproliferative disorder, intestinal camamal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early osteopetic progenitor cells with a gene, and transfer of a gene into a mammal. They are useful for treating myelofibrosis, myeloscapic osteopetics is metastatic carcinoma, acute leukaemia, myeloscapic syndions, congestive splenomegaly, Kala azar, sarcoidosis, primary theorem, congestive splenomegaly, Kala azar, sarcoidosis, primary splenic pancytopaenia, disseminated fungus disease, malaria, military tuberculosis, Fulminating septicaemia, pyridoxine deficiency syndrome) and vitiligo. The present sequence is a PCR primer which is used for an amplity particulum of the invantion of the invantion.
                                                                                                                                                                                                                                                                                                                                                                     Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal
                                                                                                                                                                                                                                                                                           Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 12C; 217pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention
                                                                                                     98US-0005243
                                                                                                                                            95US-0449653
                                                                                                                                                                                                                                                                                               Zsebo KM, Bosselman RA,
                                                                                                                                                                                     ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                        WPI; 2002-350789/38
                                                                                                                                                                                                                                                  MART/) MARTIN F H.
               US2002018763-A1.
                                                                                                                                              24-MAY-1995;
                                                                                                     12-JAN-1998;
                                                          14-FEB-2002
                                                                                                                                                                                       (ZSEB/)
(BOSS/)
(SUGG/)
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                                      Gaps
                                      ;
.5%; Score 17; DB 1; Length 20; 0.0%; Pred. No. 2.1e+02;
                                        0; Indels
      Query Match 1.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 17; Conservative 0; Mismatches
                                                                                  1084 AAAAAAAAAAAAA 1100
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18 AAAAAAAAAAAAAA 2
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ABK65035 standard; DNA; 20 BP
                                ABK65035;
RESULT 409
       ABK65035
ID ABK6
XX
AC ABK6
XX
DT 02-C
XX
DE Nanc
XX
KW Nanc
KW Nanc
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Nanoparticle-oligonucleotide #55

02-JUL-2002 (first entry)

Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection; 88.

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The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonucleotides (OGN), where OGN has a sequence complementary contracts of the sequence of NA; (b) contacting NA and NP under conditions of effective to allow hybridisation of GGN with NA; and (c) observing a detectable change brought about by hybridisation of OGN with NA.

CG detectable change brought about by hybridisation of GGN with NA.

CG The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

CC The method is useful from others and methods of nanofabrication.

CC The contract of genetic, bacterial and viral diseases. The CGN-NP conjugates diagnostic diagnostic disupplied linkers comprising a steroid residue attached to a cyclic disulphide have comprising a steroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitivity of diagnostic as the linker. The OGN-NP conjugates are stable allowing them to be used as the linker. The OGN-NP conjugates and assisting that the PCR solutions. Therefore conjugates added as probes to a DNA directly in PCR solutions. The remover and the amplicons cooling cycles of the PCR and are still able to detect the amplicons cooling cycles of the PCR and are still able to detect the amplicons conjugates and causing confamination. ABK64981-ABK65055 conjugates and constant of the ACR and causing contamination. ABK64981-ABK65055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridising nanoparticles with attached oligonuclectides to nucleic acid and detecting change brought about hybridisation -
                                                                                                                                                                                                                                                                                                                                                             Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 1.5%; Score 17; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 2.1e+02; hes 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent nanoparticle-oligonucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                           , Mucic RC, Storhoff JJ,
Li Z, Park S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 18; Page 410; 412pp; English.
                                                                                                                                                                                                         08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-0760500.
                                                                                                                                             10-AUG-2001; 2001WO-US25237.
                                                                                                                                                                                                                                                                             28-MAR-2001; 2001US-0820279
                                                                                                                                                                                                                                                                                                                                                                  Letsinger RL,
Garimella V, 1
                                                                                                                                                                                                                                                                                                                      (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-258024/30.
                                                                                                                                                                                           11-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                  G,
                                                                                                      07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                         Taton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                         Mirkin
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Nanoparticle-oligonucleotide #70. 1084 AAAAAAAAAAAAA 1100 AAAAAAAAAAAAAA 17 ABK65050 standard; DNA; 20 (first entry) 02-JUL-2002 ABK65050; RESULT 410 Matches ABK65050

Nanoparticle-oligonucleotide; nanofabrication;

0

nucleic acid detection; ss

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The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonuclectides (OGN), where OGN has a sequence complementary to the sequence of NA; (b) contacting NA and NP under conditions effective to allow hybridisation of OGN with NA.

The method is useful for detecting a nucleic acid, separating a petected nucleic acid from others and methods of nanofabrication.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and wirel diseases. The OGN-NP conjugates to essays. In particular assays using OGN-NP conjugates prepared using linkers comprising a steroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitive than assays in the linker. The OGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates added as probes to a DNA target to be PCR amplified can be carried through the 30 or 40 heating cooling cycles of the PCR and are still able to detect the amplicons without opening the tubes and causaing contemination. ABK64981-ABK65055 represent nanoparticle-oligonucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridising nanoparticles with attached oligonucleotides to nucleic acid and detecting change brought about by hybridisation
                                                                                                                                                                                                                                                                                                                                                             Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R; Garimella V, Li Z, Park S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 24; Figure 44; 412pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD14 receptor PCR primer SEQ ID NO 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL54775 standard; DNA; 20 BP
                                                                                                                                                                                                11-AUG-2000; 2000US-224631P.
08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255335P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-0820279.
                                                                                                                                                            10-AUG-2001; 2001WO-US25237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                           (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-258024/30.
                                                                             WO200218643-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-2002
                                                                                                                     07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                 Mirkin CA,
                                                                                                                                                                                                                                                                                                                                                                                     Taton TA,
                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL54775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 411
ABL54775/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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0;

0; Indels

1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02;

100.0%; Pred. No. 2.1 trive 0; Mismatches

The invention relates to a method for detecting 1 base polymorphism on the sequence of a chromosome or its fragment in which a sample nucleic acid is reacted with a reaction liquor containing a nucleic acid primer having a base adjacent to the polymorphic base at its 3'-end, one dideoxynucleotide corresponding to a polymorphic base having a distinguishable feature or its mixture, DNA polymerase and a composition required for its activity expression to detect the presence of taking dideoxynucleotide in the nucleic acid primer and to detect the type of the base to be specified. The method is used for detecting 1 base polymorphism on the sequence of a chromosome or its fragment. The present sequence is that of a PCR primer, useful in examples of the invention. Detecting 1 base polymorphism on a sequence of a chromosome or it's Oligonucleotide synthesis; polynucleotide array; protecting group; Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP; single-nucleotide polymorphism; PCR; primer; ss. Length 20; Indels Caruthers M; 1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 2.1e+02; ative 0; Mismatches 0; Oligonucleotide synthesis method related DNA #1. Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other; Perbost MGM, Betley JR, Example 2; Page 10; 10pp; Japanese. (AGIL-) AGILENT TECHNOLOGIES INC. 1084 AAAAAAAAAAAAA 1100 AAL45122 standard; DNA; 20 BP. 20 AAAAAAAAAAAAAA 4 26-JUL-2000; 2000JP-0225354. 28-JUL-2000; 2000US-0627249. 26-JUL-2000; 2000JP-0225354. 27-JUL-2001; 2001EP-0118360 24-MAY-2002 (first entry) Best Local Similarity 100. Matches 17; Conservative WPI; 2002-156732/21. WPI; 2002-275727/32 (TOYM) TOYOBO KK JP2002034599-A. oxidation; ss. Dellinger DJ, EP1176151-A1 30-JAN-2002. 05-FEB-2002 Synthetic Synthetic. AAL45122; tragment Query Match RESULT 412 AAL45122, à ö Gaps

0

Gaps

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The present invention relates to a method for the synthesis of a polynucleotide which involves coupling a second nucleoside to a first nucleoside through a phosphite linkage, where the second nucleoside has a non-carbonate protecting group protecting a hydroxyl, and exposing the product to a composition which concurrently oxidizes the phosphite formed to a phosphate and deprotects the protected hydroxyl of the second nucleoside. The method is useful for synthesizing the polynucleotides, for carrying out either 3' to 5' to 3' synthesis and for fabricating an addressable array of polynucleotides on a substrate. The present sequence is an oligonucleotide produced to demonstrate the method Synthesis of polynucleotide useful during fabrication of an array involves coupling nucleoside phosphoramidite and a solid-supported nucleoside and treating the product with an oxidation/deprotection Example 1; Page 15; 36pp; English. composition

Gaps ., 1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.16+02; cive 0; Mismatches 0; Indels Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other; Query Match Best Local Similarity 100. Matches 17; Conservative of the invention.

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0;

ABL36232 standard; DNA; 20 BP. RESULT 413 ABL36232

(first entry) 08-APR-2002 ABL36232;

M tuberculosis rRNA probe SEQ ID NO: 83.

Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis; alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic; antipsoriatic; dermatological; antiinflammatory; antiallergic; Th2 immune response; immunomodulatory; probe; ss.

Mycobacterium tuberculosis.

US6328978-B1

11-DEC-2001

99US-0324542. 02-JUN-1999;

97US-0997080 23-DEC-1997;

Prestidge R; Watson JD, Tan PLJ,

GENE-) GENESIS RES & DEV CORP LTD.

WPI; 2002-138361/18.

Inhibiting skin inflammation associated with skin disorder e.g. psoriasis, by administering composition comprising delipidated and deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae culture filtrate

5; Column 99-100; 116pp; English. Example

The present invention relates to a method of inhibiting skin inflammation associated with a skin disorder selected from psoriasis, atopic dermatitis and allergic contact dermatitis, which involves administering a composition containing delipidated and deglycolipidated Mycobacterium

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Gaps

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Indels

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1.5%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02;

ilarity 100.0%; Pred. No. 2.1 Conservative 0; Mismatches

Local Similarity les 17; Conserv

Matches

Query Match

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

٥; treated may also include alopecia areata, and skin cancers such as basal cell carcinoma, squamous cell carcinoma and melanoma. The composition acts by inhibiting the Th2 immune response. The present sequence is a probe described in the exemplification of the invention. The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cancer, colon and rectum cancer, connective tissue cancer, cesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhaddeycarcoma, skin ling or preventing cancer, such as basal cell carcinoma, comprises nistering immunostimulatory nucleic acids that induce expression of surface antigens and antibodies to a subject having or at risk of Gaps cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention. The skin disorder to be .. Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss. Length 20; 1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 2.1e+02; ative 0; Mismatches 0; Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; vaccae cells or M. vaccae culture filtrate. Immunostimulatory nucleic acid SEQ ID NO: 2. Disclosure; Page 95; 312pp; English. 1084 AAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAA 17 B 22-JUN-2001; 2001WO-US20154. 22-JUN-2000; 2000US-213346P. (IOWA) UNIV IOWA RES FOUND. ABL38648 standard; DNA; 20 17; Conservative Weiner G, Hartmann G; WPI; 2002-154611/20. Local Similarity developing cancer WO200197843-A2. administering 16-APR-2002 27-DEC-2001 Synthetic. ABL38648; Query Match Matches RESULT 414 cell ABLJ38648

ABLJ38648

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ABLJ3

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ABLJ3

ABLJ3

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ABLJ3

ABLJ3 888888 ð d

BP.

ABL39403 standard; DNA; 20

RESULT 416

ABL39403/

ABL39403;

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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, brast cancer, oconecive colon and rectum cancer, connective tissue cancer, oceophageal cancer, eye cancer, kidhey cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, nelanoma, myeloma, oral cavity cancer, ovarian nen-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                     Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      'note = "phosphorothioate backbone"
                                                                                                                                                                                                                                     Immunostimulatory nucleic acid SEQ ID NO: 838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 base= OTHER
1084 AAAAAAAAAAAAAA 1100
                                    1 AAAAAAAAAAAAA 17
                                                                                                                         ABL39402 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2000; 2000US-213346P.
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/*tag= a
                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                 /mod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-154611/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200197843-A2
                                                                                                                                                                                                                                                                                                                                                                             modified_base
                                                                                                                                                                                                 L6-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weiner G,
                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                             ABL39402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer,
                                                                                         RESULT 415
                                                                                                          ABL39402
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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, eye cancer, kidney cancer, connective tissue cancer, cesophageal cancer, eye cancer, kidney cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, stomach cancer, testicular cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in
                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                             cell lysis; cancer; immunostimulatory; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 17; DB 1; Length 20; 00.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nanoparticle-associated oligonucleotide SEQ ID 55.
                                                                                           Immunostimulatory nucleic acid SEQ ID NO: 839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. -
                                                                                                                                              angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                        22-JUN-2000; 2000US-213346P.
                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-US20154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX92177 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developing cancer
                                                                                                                           Antibody-induced
                                                                                                                                                                                                           WO200197843-A2.
                                                            16-APR-2002
                                                                                                                                                                                                                                           27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                        Weiner G,
                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX92177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 417
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Gaps

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1084 AAAAAAAAAAAAA 1100

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20 AAAAAAAAAAAAAA 4

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Nonoparticle, nucleic acid detection, hybridisation, diagnosis, sequencing, viral infection; human immunodeficiency virus; HIV, hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus; bacterial infection; sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication; gene therapy; ss.
                                                                                                                                                                                                                                                                                                    Detecting nucleic acids having at least two portions involves use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence
                                                                                                                                                                                                                                                  Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 59; 130pp; English.
                                                                                                                                                              26-APR-2000; 2000US-200161P.
26-UUN-2000; 2000US-0603830.
21-UUL-1997; 97WO-US12783.
                                                                                                                                                     96US-031809P
                                                                                                                                                                                             99US-0240755
                                                                                                                              28-SEP-2001; 2001US-0967409
                                                                                                                                                                                                                             (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                 WPI; 2003-182627/18.
                                                                                    JS2002155458-A1.
                                                                                                                                                                                                         25-JUN-1999;
                                                                                                                                                   29-JUL-1996;
                                                                                                                                                                                               29-JAN-1999;
                                                                                                         24-OCT-2002
                                                                Synthetic
                                                                                                                                                                                                                                                            Taton TA;
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This invention describes a novel method of detecting nucleic acid having at least two portions. The method involves providing nanoparticles at least two portions. The method involves providing nanoparticles catached to oligonucleotides, where the oligonucleotide on each nanoparticle have a sequence complementary to a sequence of at least two portions of nucleic acid, contacting nucleic acid and nanoparticle to callow hybridisation of the oligonucleotide on the nanoparticle with two or more portions of nucleic acid and observing a detectable change contacting about by hybridisation of the oligonucleotide nanoparticle with nucleic acid having at least two portions, from other nucleic acids and for acid having at least two portions. The method is useful for detecting nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids preferably, the method is useful for detecting nucleic acids for diagnosis and/or molitoring of viral infections (human immunodeficiency virus (HIV), hepatitis virus, herpes virus, conformative and Epstein-Barr virus), chatterial diseases, sexually transmitted diseases, inherited disorders, and for monitoring gene therapy. The method is useful in research and analytical laboratories in DNA sequencing, in the field to cates the presence of specific pathogens. Detecting nucleic acids based on observing a colour change with the naked eye is cheap, fast, simple and robust and does not require specialised expensive equipment.
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                                                                                     Gaps
                                                                                     ;
                                        1.5%; Score 17; DB 1; Length 20; 00.0%; Pred. No. 2.1e+02;
                                                                                  0; Indels
Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
                                                       Best Local Similarity 100.0%; Pred. No. 2.1 Matches 17; Conservative 0; Mismatches
                                          Query Match
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1084 AAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAA

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Nanoparticle, 88, nucleic acid detection; viral disease, probe; human immunodeficiency virus infection; hepatitis virus infection; herpes virus infection; oytomegalovirus infection; foreneic science; Beptein.Barr virus infection; bacterial disease; gene therapy; sexually transmitted disease; inherited disorder; DNA sequencing; paternity testing; cell line authentication.
                                                                                                                                                                                                                                                                                                                                                                          Detecting nucleic acids having at least 2 portions comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence -
                                                                                                                                                                                                                                                                                                                          Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 18; Page 44; 130pp; English.
                                                          Thio-modified 20dA oligonucleotide.
ABX79181 standard; DNA; 20 BP
                                                                                                                                                                                                                                 96US-031809P.
2000US-200161P.
2000US-0603830.
                                                                                                                                                                                                              12-OCT-2001; 2001US-0976577.
                                                                                                                                                                                                                                                              97WO-US12783
                                                                                                                                                                                                                                                                                   99US-0344667.
                                      15-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                      (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-198491/19.
                                                                                                                                                                     US2002155462-A1.
                                                                                                                                                                                                                                 29-JUL-1996;
26-APR-2000;
                                                                                                                                                                                                                                                     26-JUN-2000;
                                                                                                                                                                                                                                                               21-JUL-1997;
                                                                                                                                                                                                                                                                          9-JAN-1999;
                                                                                                                                                                                                                                                                                  25-JUN-1999;
                                                                                                                                                                                          24-OCT-2002
                                                                                                                                                                                                                                                                                                                        Mirkin CA,
                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                    Taton TA;
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The invention relates to detecting a nucleic acid (NA) having at least 2 portions, comprises providing a type of nanoparticles (NP) having catached to oligonucleotides (O) (O) on each NP has a sequence of attached to oligonucleotides (O) (O) on each NP has a sequence of an each NP has a sequence of an each NP is a sequence of an each NP is contacting NP. The nanoparticle is useful for separating a selected on NP with NA. The nanoparticle is useful for separating a selected nucleic acid having at least 2 portions. The method of consing NP is useful for detecting any type of nucleic acids and for detecting nucleic acids having at least 2 portions. The method of used for detecting nucleic acids in sequencing on the method of using NP is useful for detecting on the each of disease and in sequencing of nucleic acids for used for diagnosis of disease and in sequencing of nucleic acids for Preferably, the method is useful for detecting nucleic acids for virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus, bacterial diseases, sexually transmitted diseases, inherited discretion and for monitoring gene therapy. The method is useful in research and analytical laboratories in DNA sequencing and in the field to detect the presence of specific pathogens. Detecting nucleic acids barricles and robust, and do not require specialised expensive equipment. The present sequence is a nanoparticle (e.g. gold in remains) and probe used to demonstrate the method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Gaps · 0 Length 20; Indels Query Match
1.5%; Score 17; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 2.18+02;
Matches 17; Conservative 0; Mismatches 0;

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us09904568-1.rng

Page 188

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/mod
                                                                     WPI; 2003-157021/15.
                                              WO2002102815-A2
                                   Key
modified_base
                                                                 Ravikumar VT;
                    08-APR-2003
                                                                              enantiomer
                               Synthetic.
                ABZ22916;
         RESULT 419
          ABZ22916/
                ò
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Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss. 'note = "phosphorothioate linkages" Phosphorothioate 20-mer oligonucleotide #1. Location/Qualifiers base= OTHER 1084 AAAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAAA 17 ABZ22916 standard; DNA; 20 BP 13-JUN-2002; 2002WO-US18581 .4-JUN-2001; 2001US-0881535. (first entry) /*tag= a (ISIS-) ISIS PHARM INC.

The present invention describes a method (M1) for preparing an internucleotide phosphorothioate linkage enriched in the Sp or Rp canticular between a synthon having a hydroxyl moiety at the 5' position and a 2'-substituted nucleoside having an activated phosphate moiety at the 3'-position, comprising coupling a synthon with a 2'-substituted nucleoside in the presence of coupling agent that is selected to enhance continue and the sp or Sp enantiomer according to its pKa. This method is circumstant for preparing an oligonucleotide having at least one region of internucleotide linkages that is enhanced in the Sp or Rp enantiomer, which involves providing a nucleotide having a hydroxyl moiety of the 5'-position or a growing oligonucleotide chain having a hydroxyl moiety of the 5'-position or a growing oligonucleotide chain having a hydroxyl moiety of the 5'-position in the presence of the coupling agent, and repeating the coupling step until the desired number of linkages is capabilished. The oligonucleotide having a region of internucleotide continue another region of internucleotide linkages that is enhanced in the Sp enantiomer is further processed to include another region of internucleotide linkages that is enhanced in the Sp and/or Rp enantiomer. Oligonucleotide linkages that is enhanced in the Sp and/or Rp enantiomer. Oligonucleotide sprepared by the method lead to improved drugs, diagnostics and research reagents. The present of the harmagent invantion Preparing internuclectide phosphorothicate linkage enhanced in Sp/Rp enanticmer, by coupling a synthon with 2'-substituted nucleoside in presence of coupling agent having a pKa that enhances linkage in Sp/Rp Example 1; Page 31; 65pp; English

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

the present invention.

Length 20;

1.5%; Score 17; DB 1;

Query Match

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0; Gaps

th 1.5%; Score 17; DB 1; Length 20; Similarity 100.0%; Pred. No. 2.1e+02; 17; Conservative 0; Mismatches 0; Indels

Best Local Similarity

Query Match Matches

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The invention relates to DNA sequences (I) that encode six specific plant correins: (i) a protein (ABP60425) with mitochondrial carrier protein cativity (IIa); (ii) a protein (ABP60420) with transferrin binding protein activity (IIb); (iii) a protein (ABP60429) with receptor-like protein kinase activity (IIb); (iv) a protein (ABP60429) with horiong cartivity (IIb); (iii); (iv) a protein (ABP60429) with horiong factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long cernical repeat retroelement reverse transcriptase activity (IIe); or (vi) a protein (ABP60430) with helicase activity (IIf); (I), also related sequences, extression vectors, encoded proteins and antibodies against the proteins, are used to produce plants with altered properties, including tolerance of overwatering. The cartivodries are also used for isolation of the proteins and in in incluminates and constitutively, aerobically or anaerobically confinents. Since (I) are derived from potato, their promoters and the confidence that encodes (IId) is used to alter the translation profile in confinents. Since (I) are derived from potato, their promoters and improved tissue specifically for use in potato, with confinence expression in potato, with improved tissue specificity and inducibility, and can also be used to control endogenous genes. The present sequence is that of a PCR primer control endogenous genes. The present sequence is that of a PCR primer control endogenous genes. The present sequence is that of a PCR primer control endogenous genes. The present sequence is that the control.
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                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
                                                                                                                                                                                                                                                                                                                                                                                                                        transferrin binding protein; receptor-like protein kinase; helicase; non-long terminal repeat retroelement reverse transcriptase; overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
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                                                                 1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2001; 2001DE-1014063.
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                                                                                                                                                                                                                                                                                                                                                              Potato gene PCR primer dT20.
                                                                                                                                                                                                                         ABZ59815 standard; RNA; 20
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Best Local Similarity 100.0
Matches 17; Conservative
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q7578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                       Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
                                                               Reverse transcription primer used in cDNA analysis technique.
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                           (first entry)
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                                                                                                                                                                                                                                                                                                   CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device; SAED; hybridisation; ss.
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                                                                                                                                                                                                                                                           CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
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/note= "3' ribonucleoside terminal"
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1084 AAAAAAAAAAAAAA 1100
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                         Length 21;
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1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0;
Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;
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                                                                   1084 AAAAAAAAAAAAA 1100
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ID AAQ75735 standard; DNA; 21
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                                                          cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 0;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVSST-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;
                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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tes 17; Conserv
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followed by
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aggregate;
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Matches
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcribtion primers (GENESED files PAG7554-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                                                                                                                                                                                      1.5%; Score 17; DB 1; Length 21;
100.0%; Pred. No. 2.3e+02;
live 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                     Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 17; Conservative
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1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02; cive 0; Mismatches 0; Indels

AAQ75741 standard; DNA; 21 BP

AAQ75741/

(first entry)

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AAQ75741;

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
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Best Local Similarity 100..
These 17; Conservative
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16-APR-1993;
                                         16-APR-1993;
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                                                                                                                                                                                                                          gene expression; reverse transcription; primer; cDNA;
restriction enzyme; 88.
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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Disclosure; Page 8; 11pp; Japanese.

WPI; 1995-018287/03.

93JP-0112515. 93JP-0112515.

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aggregate;

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Best Local Similarity

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Query Match

BP.

AAQ75742 standard; DNA; 21

AAQ75742/c RESULT 430

(first entry)

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    04-AUG-1995 (first entry)
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seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                expression; reverse transcription; primer; cDNA;
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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                                         Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
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ID AAQ75746 standard; DNA; 21 BP.
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Best Local Similarity
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              rapidly and easily
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Best Local 9
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AAQ75745/c
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Matches
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as th template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                                                                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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Reverse transcription primer used in cDNA analysis technique
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0;
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                                                                     Disclosure, Page 8; 11pp; Japanese.
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(first entry)

gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.

93JP-0112515 93JP-0112515 1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02;

Query Match Best Local Similarity

BP; 1 A; 2 C; 1 G; 17 T; 0 other;

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Length 21; Indels

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Analysis, gene expression, reverse transcription, primer, cDNA, aggregate, restriction enzyme; ss.
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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(first entry)

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                                 and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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amplification of

cDNA and gene expression - by ampl digestion with restriction enzymes

93JP-0112515 93JP-0112515 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

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                                                                                    Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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AAQ75789 standard; DNA; 21 BP.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction separate lanes. The method can be used to analyse gene expression rapidly and easily.
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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Matches 17; Conservative 0; Mismatches 0;
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                                                                          Disclosure; Page 9; 11pp; Japanese
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNSSEQ files AAQ75547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
and a plural type of labelled reverse transcription primers (GENESDE files AAQ75579) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.
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100.0%; Pred. No. 2.3e+02;
rative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity
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AAQ75773 standard; DNA; 21 BP.
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Disclosure; Page 9; 11pp; Japanese.
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Best Local Similarity
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AAQ75778/c
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1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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         AAQ75775 standard; DNA; 21 BP.
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Pred. No. 2.3e+02;
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100.0%; Pred. No. 2.
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RESULT 454 **AA**Q75779,

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSED files AAQ/5547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                    Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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Reverse transcription primer used in cDNA analysis technique.
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AAQ75781 standard; DNA; 21
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Best Local Similarity
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followed by digestion with restriction enzymes

Disclosure; Page 9; 11pp; Japanese.

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                                                             A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) (Ises AAQ75547-Q7588) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled creverse transcription primers primers (GENESE) files AAQ75547-Q7798) and using the aggregate of mRNAs as th template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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(GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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RESULT 462 AAQ75767/c

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AAQ75767 standard; DNA;

(first entry)

93JP-0112515 93JP-0112515

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded CDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                 Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                       Reverse transcription primer used in cDNA analysis technique.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily. A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q7759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression Gaps Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss. Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes 0; Reverse transcription primer used in cDNA analysis technique Query Match 1.5%; Score 17; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other; (NITE) NIPPON TELEGRAPH & TELEPHONE CORP (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. Disclosure, Page 9; 11pp; Japanese. Disclosure; Page 9; 11pp; Japanese. 1084 AAAAAAAAAAAAA 1100 BP. 93JP-0112515. 93JP-0112515 17 AAAAAAAAAAAAAAA AAQ75769 standard; DNA; 21 (first entry) WPI; 1995-018287/03. WPI; 1995-018287/03 rapidly and easily. JP06303997-A. 16-APR-1993; 16-APR-1993; 04-AUG-1995 01-NOV-1994 aggregate; Synthetic. Analysis; AAQ75769; RESULT 464 AAQ75769, g

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1.5%; Score 17; DB 1; Length 21; ilarity 100.0%; Pred. No. 2.3e+02; Conservative 0; Mismatches 0; Indels

expression; reverse transcription; primer; cDNA;

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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100.0%; Pred. No. 2.3e+02;
Ative 0; Mismatches 0;
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                                  1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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tive 0; Mismatches 0; Indels
Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;
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                                  A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNSSEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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Matches 17; Conservative 0; Mismatches 0;
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Disclosure; Page 7; 11pp; Japanese.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVIS-Y-QTSTS) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction elzyme and; (c) electrophorealing the digested aggregate of cDNAs in separate lames. The method can be used to analyse gene expression
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Reverse transcription primer used in cDNA analysis technique.
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AAQ75607 standard; DNA; 21 BP
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template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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AAQ75609/c
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-Q75788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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100.0%; Pred. No. 2.3e+02;
ative 0; Mismatches 0;
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            Score 17; DB 1; Length 21; Pred. No. 2.3e+02; 0; Mismatches 0; Indels
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Disclosure; Page 6; 11pp; Japanese

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                               A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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(first entry)

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ7554-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
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AAQ75617 standard; DNA; 21 BP.
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Les 17; Conservative
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                                                                           rapidly and easily
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AAQ75617/c
ID AAQ756
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16-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                     gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
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                                    Reverse transcription primer used in cDNA analysis technique
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                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                        Disclosure; Page 6; 11pp; Japanese
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                   (first entry)
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                                                      Analysis; gene
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                   04-AUG-1995
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                                                              aggregate;
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AAQ75617;
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
                                                                     Analysis of cDNA and gene expression - by amplifollowed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
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WPI; 1995-018287/03.
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Best Local Similarity
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-extranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
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                    aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                          Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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llarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0; Indels
                 Length 21;
                                                 0; Indels
               DB 1; Le: 2.3e+02;
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             Score 17; DB :
Pred. No. 2.3
0; Mismatches
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ID AAQ75621 standard; DNA; 21
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                                                   Conservative
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       Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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AAQ75621;

RESULT 488

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Best Loca Matches

Synthetic

AAQ75620

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Gaps

Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

JP06303997-A.

Synthetic.

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Gaps

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Length 21; Indels 01-NOV-1994.

Reverse transcription primer used in cDNA analysis technique.

(first entry)

04-AUG-1995

AAQ75661

BP.

AAQ75661 standard; DNA; 21

AAQ75661/c

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENDESEQ files AAQVSST4-QYSPS) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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100.0%; Pred. No. 2.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                             1.5%; Score 17; DB 1; Le:
100.0%; Pred. No. 2.3e+02;
Ltive 0; Mismatches 0;
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Best Local Similarity
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQTSSTQ-705798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                          cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
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Local Similarity 100. 188 17; Conservative

Best Loca Matches

17 AAAAAAAAAAAAAA

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Gaps

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Length 21;

1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) illes AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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Best Local Simi:
Matches 17; (
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followed by
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enzyme and; (c) electrophoresing the digested aggregate of cDNAs seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reverse transcription primer used in cDNA analysis technique.
                                                                                                Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restriction enzyme; ss.
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Best Local Similarity 100.(
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AAQ75645/
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                                                                                                                                                                                                       CDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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Pred. No. 2.3e+02;
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100.0%; Pred
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                      Synthetic,
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                                                                                                                                                                                                                      expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                aggregate; restriction enzyme; ss
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription priners (GENESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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Page 216

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                Analysis; gene expression; reverse transcription; primer; cDNA, aggregate; restriction enzyme; ss.
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                              Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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          (first entry)
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A method for the analysis of cDNA comprises (a) preparing an anggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) alectrophorealing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                               of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
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ID AAQ75649 standard; DNA; 21
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Best Local Similarity 100.
Matches 17; Conservative
WPI; 1995-018287/03
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                                               Analysis (followed)
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Length 21;

DB 1;

Score 17;

1.5%;

Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 other;

100.08;

Best Local Similarity

Matches

à 셤 AAQ75650,

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the temptate for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreship the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
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AAQ75652 standard; DNA;
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Matches 17; Conserv
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Pred. No. 2.3e+02;
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100.0%; Pred. No. 2.3e+02;
Live 0; Mismatches 0; Indels
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                                   Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded CDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
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AAQ75653 standard; DNA; 21 BP.
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Best Local Similarity 100.
Matches 17, Conservative
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                                                                                                                         expression; reverse transcription; primer; cDNA;
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                                                                                                             Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                      aggregate; restriction enzyme; ss.
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                          AAQ75654 standard; DNA; 21
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Best Local Similarity 100.
Matches 17; Conservative
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RESULT 502
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                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
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0; Mismatches
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                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                           Disclosure; Page 6; 11pp; Japanese
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                                                                   WPI; 1995-018287/03
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                                                                                                                                                                                                                                          rapidly and easily.
                      16-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggregate;
                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ75656,
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75247-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                            Gaps
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seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 2.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                   Length 21,
                                                                                                                                                                                                      Indels
                                                                                                                                             1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
                                                                                    Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                            1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                  17 AAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                      17; Conservative
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Matches 17; Conservative
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                                                                                                                                       Query Match
Best Local Similarity
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1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                               Oligonucleotide probe, CP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0271882
                                                                                                                                                                                                                                      17 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                      AAT10743 standard; RNA; 21
                                                                                                                                                                                                                                                                                                                           09-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans GA, Heller MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-097582/10.
                                                                                                                                        rapidly and easily
                                                         A method for the
                                                                                                                                                                                                                                                                                                                                                                                                                                   modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                          AAT10743;
                                                                                                                                                                                                                                                                    RESULT 508
                                                                                                                                                                                                                                                                              AAT10743
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                                                                                                                                                                                                                                                    A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and, (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                       Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                      yene expression, reverse transcription; primer; cDNA; restriction enzyme; ss.
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                 Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 2.3e+02;
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100.0%; Pred. No. 2...
... 0; Mismatches
                                                                                                                                                                 (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                    Disclosure; Page 6; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAA 1100
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(first entry)
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                                      Analysis; gene
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                                                                                                       01-NOV-1994
                                                 aggregate;
                                                                  Synthetic
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENBSEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded CDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                               comprises (a) preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "3'-ribonucleoside terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
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                                                                                                                             Disclosure; Page 6; 11pp; Japanese.
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Gaps

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Length 21; 0; Indels

This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygoty (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a present condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells and the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can normal somatic cells, and the first gene. The products and methods can normal search and adaptication and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney permeable to a counterion but not permeable to a molecule capable of insultating or binding to the electrode. The attachment layer is capable of attaching a accromolecule. The ED is used for genetic typing and comprises a number of electronically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence. Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other; 1084 AAAAAAAAAAAAAA 1100 1 AAAAAAAAAAAAAAAA 17 20-MAR-1997; WO9841648-A2 19-MAR-1998; 30-NOV-1999 24-SEP-1998 Housman D, AAZ26268; RESULT 509 Ношо AAZ26268/ 22222222 ð 셤

Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumaning, polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss. Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plague, dysplastic lesions, endometriosis or graft versus host disease Disclosure; Figure 7; 605pp; English Ledley FD, Stanton VP; BP. Human polymorphic region 457. 97US-0041057. 98WO-US05419. AAZ26268 standard; DNA; 21 (first entry) VARI-) VARIAGENICS INC WPI; 1998-521232/44.

. 0 recombinant vaccinia virus comprising of a gag gene from a retrovirus such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope region (30-300 bases in length) of a retroviral gene other than the gag gene may be altered so as to produce a gag protein modified from the natural sequence by the addition, deletion or substitution of at least 1 amino acid residue. The fusion gene is inserted into a region of a vaccinia virus not essential to its propagation, to give a recombinant vaccinia virus vector which is used to transform a host cell (such as Hela, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon qulturing the host cell produces particulate structures containing the fusion gag protein. The recombinant vaccinia virus or the fusion gag protein gag in the production of vaccines for region; ENV protein; vaccinia virus; gag gene; retrovirus; disease, and graft versus host disease. The method can also be used tremove malignant cells from bone marrow transplants. AAZ25812-Z26825 represent human polymorphic sites described in the method of the Gaps Recombinant vaccinia virus containing fusion HIB gag gene - for production in host cells of gag protein for use as vaccine .; AAV35388-V35414 are primers used in a method which results in 0; Indels Length 21; Score 17; DB 1; Le Pred. No. 2.3e+02; Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 other; vaccines; infection; protection; primer; ss. NINA-) JAPAN NAT INST INFECTIOUS DISEASES. Mismatches Example 1; Page 66; 84pp; Japanese. Similarity 100.0%; Pr HIV-1 gag protein DNA primer #8 1081 ATTAAAAAAAAAAA 1097 19 ATTAAAAAAAAAA 3 97WO-JP04216 96JP-0323412. AAV35395 standard; DNA; 21 13-OCT-1998 (first entry) JAPG) NIPPON ZEON KK Kurata T, WPI; 1998-312481/27. Hypervariable 19-NOV-1996; 19-NOV-1997; Local Sam WO9822596-A1 28-MAY-1998. Kojima A, Synthetic. AAV35395; Query Match RESULT 510 Matches AAV35395 ប្រក្តិប្តិក្តុស្តី à d

Gaps 0 Length 21; 1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Sequence 21 BP; 19 A; 2 C; 0 G; 0 U; 0 other; 17; Conservative Best Local Similarity Query Match Matches à

protecting against infection with retroviruses such as HIV

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1084 AAAAAAAAAAAAA 1100

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The specification describes a self-addressable, self-assembling microelectronic device which is designed to actively carry out and control multi-step and multiplex molecular biological reactions in microscopic formats. A key aspect of this inventions is played by the incremeable permeation layer which overlies the electrode. This incremeation layer allows attachment of nucleic acids to permit immobilization but also separates the attached oligonuclectices and hybridized target DNA sequences from the highly reactive electrochemical whybridized target DNA sequences from the highly reactive electrochemical control described is mediately at the electrode surface. The microelectronic device is designed and fabricated to actively carry out and control reactions, sample preparation, diagnostics and biopolymer synthesis. The device can electronically control the transport and attachment of specific micro-locations. The device can cids and polypeptides, to specific micro-locations of analytes or reactants of the addressed specific micro-locations. The device can at the addressed specific micro-locations. The device can concentrate analytes and reactants, remove non-specifically bound molecules, provide stringency control for DNA hybridization reactions of molecules, provide stringency control for DNA hybridization reactions represent sequence.
                                                                                                                                                                                         Microelectronic device; multi-step reaction; microscopic format; ion-permeable permeation layer; electrode; electrical control; transport; attachment; binding; DNA/RNA hybrid; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heller MJ, Nerenberg MI, Sosnowski RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New microelectronic device designed to carry out and control multi-step and multiplex molecular biological reactions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.5%; Score 17; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a probe used to exemplify the invention
                                                                                                                                                    3' ribonucleoside oligonucleotide probe CP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 89; 179pp; English.
                                     AAX81302 standard; DNA; 21 BP
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Butler WF, Edman CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NANO-) NANOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-385567/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microscopic format
                                                                                                                   20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                         WO9929711-A1
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                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                    misc RNA
RESULT 511
                    AAX81302
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mammary-specific protein, designated mammaglobin. The specification by Beacribes a protein comprising a mammaglobin antigen that is recognized by B and/or To cells specific for the natural, secreted and glycosylated form of mammaglobin polypeptide. This protein, or recombinant vectors that express it, are used in vaccines for treating mammaglobin-expressing cancers, specifically of the breast. Such cancers can also be treated using autologous tumor lymphocytes activated ax vivo with an mammaglobin antigen, then returned to the patient. Expression of mammaglobin is elevated in 27% of stage I primary breast cancers, so it represents a marker useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present primer was used to reverse transcribe RNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                           Human; mammary-specific protein; mammaglobin; antigen; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammaglobin, secreted protein overexpressed in breast cancer
                                                                                                                                                                                                                                           mammaglobin-expressing cancer; breast cancer;
autologous tumor lymphocyte; diagnosis; marker; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 17; DB 1; Length 21;
100.0%; Pred. No. 2.3e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                              Primer used to reverse transcribe mammaglobin RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase inhibiting primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 55; 60pp; English.
1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAAA 1100
                                                                                                      AAX26973 standard; cDNA; 21 BP
                            1 AAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AAAAAAAAAAAAAA 5
                                                                                                                                                                                                                                                                                                                                                                                                                97US-0933149.
                                                                                                                                                                                                                                                                                                                                                                                   98WO-US17991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ44350 standard; DNA; 21
                                                                                                                                                                25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of this disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-244021/20.
                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                8-SEP-1997;
                                                                                                                                                                                                                                                                                                                    WO9914230-A1
                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleming TP,
                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                    AAX26973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ44350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 513
AAZ44350/C
ID AAZ4431
XX
AC AAZ4431
XX
DT 04-APR
DX
DX
XX
                                                                                         AAX26973
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Gaps

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                                                                                                                                                                                                                                                                                                                                                       This invention describes novel purified aptameric oligonucleotides which have antimicrobial, cytostatic and immunosuppressive activity. The oligonucleotides are useful for binding to and preventing or inhibiting the biological function of a protein kinase or a target molecule and for detecting the presence or absence of a target molecule and for detecting the presence or absence of a target molecule in biological samples. The oligonucleotides are also useful for prophylactic and therapoutic treatment of diseases such as cancer, autoimmune diseases and diseases caused by pathogenic microorganisms. This sequence represents a primer used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Branched chain compound; nucleic acid synthesis; primer extension; reverse transcription; nucleic acid hybridization; nucleic acid amplification; ss.
                                                                                                                                                                                                                                                                                       Oligonucleotides inhibiting protein kinase, useful for treating diseases such as cancer and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
 Antimicrobial; cytostatic; immunosuppressive; protein kinase; prophylactic; therapy; treatment; cancer; autoimmune disease; pathogenic microorganism; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide used to produce branched chain compounds.
                                                                                                                                                                                                                                                                                                        autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                      & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "NH2-C6 attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6..7
/*tag= c
/note= "branch present"
                                                                                                                                                                                                                                                                                                                              Example 8; Column 27-28; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100
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"NH2-C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                              95US-0416214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                  (USSH ) US DEPT HEALTH
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                                                                                                                                                                                                                                Bergan R, Neckers L;
                                                                                                                                                                                                                                                           WPI; 2000-104623/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified base
                                                                                                                                            14-APR-1995;
                                                                                                                                                                       04-APR-1995;
                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                   US5998596-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001
                                                                                                                 07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH42480;
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AAH42480/c
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Vaccine, cytostatic; virucidal; bactericidal, fungicidal, anti-parasitic; immunostimulatory, tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothicate; ss.
                                                                                                                                                                                                         Gaps
                                                                                                                                                         Branched compounds useful in e.g. nucleic acid synthesis reaction comprises nucleic acid moieties optionally extended by a polymerase
                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                      Query Match
1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                               Schmidt W, Hiller R, Huber M, Mueller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid #823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krieg AM, Schetter C, Vollmer J;
                                                                                                                                                                                          Example 1; Page 10; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF99707 standard; DNA; 21 BP.
                                        99EP-0125484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1999; 99US-0156113.
27-SEP-1999; 99US-0156135.
23-AUG-2000; 2000US-0227436.
                                                             99EP-0125484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2000; 2000WO-US26383
                                                                                (LION-) LION BIOSCIENCE AG. (VBCG-) VBC GENOMICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                     21 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-2001 (first entry)
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(COLE-) COLEY PHARM GMBH
                                                                                                                                     WPI; 2001-466959/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200122972-A2.
EP1111068-A1
                                       21-DEC-1999;
                                                             21-DEC-1999;
                   27-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF99707;
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AAF99707/c
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Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #912.
                                                                                                                             Query Matcn
Best Local Similarity 100.0%; Pred. No. 2.3
                          Claim 101; Page 56; 338pp; English.
                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                   (COLE-) COLEY PHARM GROUP INC.
                                                                                                                                                                                       ABS78428 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                               14-DEC-2001; 2001WO-US48458
                                                                                                                                                                                                                                                                                                                         14-DEC-2000; 2000US-255534P.
                                                                                                                                                           21 AAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                         40200253141-A2
                                                                                                                                                                                                                                                                                                                                              Bratzler RL;
                                                                                                                                                                                                            13-DEC-2002
                                                                                                                                                                                                                                                                                                     11-JUL-2002.
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                            Query Match
                                                                                                                                                                                 ABS78428,
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(first entry)

Claim 2; Page 35; 276pp; English.

WPI; 2002-566690/60.

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule.

Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, errolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiolibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody-induced cell lysis, cancer, immunostimulatory, CD20, angiogenesis, metastasis, cytostatic, phosphorothicate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                 sequence is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%; Score 17; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid SEQ ID NO: 840.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL39404 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AAAAAAAAAAAAA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-154611/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200197843-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                          The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae haemophilus, campylobacter, clostratium, scherchia coll and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is slow useful for preventing cancer, asthma, infectious disease, allergy or immune deliciency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells.

Note: the present sequence may have a phosphorothicate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myoccardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound gramulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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The invention relates to a method for assessing a condition of a performance animal. The method involves determining in sample abundance of expressed target nucleic acid; transmitting digital sample signal at remocely remote diagnostic server; processing digital sample signal at remocely located database to correlate digital signal with digital information and returning report of particular condition of animal. The method is useful for assessing a condition of a performance animal preferably human, dog or camel. The condition can be an athletic ability and a condition that enhances, hinders, impedes or does not change an expected ability of the performance animal; and also normal, pre-clinical, overt progress and/or stage of disease, undiagnosed of unclassified conditions, presence of drugs, response to exercise, response to vaccines, therapies, nutritional states and response to environmental conditions. Diseases assessed by the invention include laminitis, lameless, viral or bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis; gastritis; gastric ulcer; respiratory allment; fracture; joint disease; musculoskeletal damage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regular oligo dT primer used to illustrate the method of the invention.
cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eve cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, rhabdomyosarcoma, skin present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing condition e.g. athletic ability, stage of disease, presence of drugs, response to exercise, response to vaccines, therapies, nutritional states, of performance animal involves analyzing nucleic
                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                              1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                            Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOMICS RES PARTNERS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 46; 87pp; English.
                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2001; 2001AU-0004809.
29-JUN-2001; 2001US-0896941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-2002; 2002WO-AU00553.
                                                                                                                                                                                                                                                                                                                                                                       21 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD51323 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-120558/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD51323
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD51323/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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disease, gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis, musculoskeletal damage or disorders and joint diseases. The present sequence is a primer used to illustrate the method of the
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                          antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
RNA cleavage; antiviral therapy; chimeric molecule; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is an example of a 2-5A-antisense oligonucleotide chimeric molecule. The antisense region targets the chimeric molecule. The antisense region of RNA to be specifically cleaved and the 2',5'-linked tetradenylate tail activates the 2-5A RNase. Typical applications are treatment of viral infections (esp. for cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular disorders (e.g. restenosis after angloplasty), genetic disorders, osteoarthritis or rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specific cleavage of RNA, useful partic. for treating viral infection, cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator of 2-5A dependent RNase
                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                               2',5'-linked tetraadenylate-antisense oligonucleotide chímeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/label= 2'.5'-linked tetraadenylate
/note= "nucleotides linked through phosphodie
bonds at hydroxyl groups of 2' and 5'
                                                                                                       Length 21;
                                                                                                                               0; Indels
                                                                                                    1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torrence P;
                                                                       Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5..22
/*tag= b
/note= "antisense region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                              AAQ64706 standard; cDNA to mRNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lesiak K, Maitra R, Silverman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLEV-) CLEVELAND CLINIC RES INST
                                                                                                                                                             1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                       21 AAAAAAAAAAAAA 5
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                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-151315/18.
                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1992;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9409129-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-1994.
                                                                                                                                                                                                                                                                                                                     25-MAR-2003
04-JAN-1995
                                             invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                         AAQ64706;
                                                                                                    Query Match
                                                                                                                               Matches
                                                                                                                                                                                                                                               AAQ64706/
                                                                                                                                                                                                                                   RESULT
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Gaps

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Length 22; 0; Indels

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"the 2-5A moiety (*tag = a) and the antisense
DNA sequence (*tag = c) are linked by two
1,4-butanediol molecules linked through
phosphodiester bonds"
                                                                                                                                                                                                                                                                                                             2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was used to determine whether 2-5A-antisense chimeric molecules are inhibitory to cell growth. The molecules AAQ64709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= a
/label= 2.,5'-linked tetraadenylate
/note= "nucleotides linked through phosphodiester
/note= thydroxyl groups of 2' and 5'
carbons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c
"antisense region, complementary to oligo
                                                                                                                                                                                                                                                                                                                                      antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator; RNA cleavage; antiviral therapy; chimeric molecule; PKR; protein synthesis regulation; phosphorylation; eIF-2alpha; eukaryotic translation initiation factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Specific cleavage of RNA, useful partic. for treating viral infection, cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator of 2-5A dependent RNase
                                                               Score 17; DB 1; Le
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Torrence P;
arthritis. (Updated on 25-MAR-2003 to correct PN field.)
                                      Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 other;
                                                              Query Match
1.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2.4.
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CLEV-) CLEVELAND CLINIC RES INST.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                AAQ64724 standard; cDNA to mRNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silverman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 66; 86pp; English.
                                                                                                                     1084 AAAAAAAAAAAAAA 1100
                                                                                                                                              22 AAAAAAAAAAAAAA 6
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                                                                                                                                                                                                                                                                     (updated)
(first entry)
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/*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maitra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-151315/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc feature
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                                                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                04-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1994,
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                                                                                                                                                                                                                                           AAQ64724;
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                     RESULT 520
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This invention describes a novel method of determining a predisposition to disease by genotyping a subject's DNA sequence (A) of the human mismatch repair gene, MSH6 at specified positions and comparing with reference DNA sequences, optionally taking into account all possible combinations of variations of the individual mutations, including any chosen absolute number of variations. (A), and analysis of their sequences, are useful for the following: (i) determining an increased mutation rate (frequency of base substitutions, insertions and/or deletions) in eukaryotic cells; (iii) predicting the progression, severity and survival time of patients with neoplastic disease; (iv) the development of therapeutic and 'life-style' choplastic disease; (iv) the development of therapeutic and 'life-style' drugs; (v) predicting individual differences in response to known chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv); (vi) optimizing individual treatments and interventions against neoplasia; (vi) controlling the mutation rate in eukaryotic cells, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel variants of the human mismatch repair gene, MSH6, useful e.g. for determining predisposition to cancer and for development of drugs -
                 2-5A-antisense oligonucleotide chimeric molecules, the antisense region targets the chimeric molecule to a particular region of RNA to be specifically cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A RNBse. Typical applications are treatment of viral infections (esp. for cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular disorders (e.g. restenosis after angiography), genetic disorders, osteoarthritis or rheumatoid
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mismatch repair gene; hMSH6; disease predisposition; genotype;
mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
neoplastic disease; drug development; ss.
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    In the novel
                                                                                                                                                                                                                                                                   Length 22;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human mismatch repair gene hMSH6 intron 9 DNA fragment.
                                                                                                                                                                                                                                                               1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
    cytotoxicity.
                                                                                                                                                                                  (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                           Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plaschke J, Kruppa C, Schackert H;
AAQ64711 and AAQ64724 all lacked
                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 4; 14pp; German.
                                                                                                                                                                                                                                                                                                                                                                                        1 AAAAAAAAAAAAA 17
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity luv..
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-588378/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA98276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA98276,
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Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss. Oligomer IL6805 for forming triplex with HUMIL6 target duplex.

Synthetic.

AAQ30432 standard; DNA; 23 BP

AAQ30432,

(updated)

25-MAR-2003 07-DEC-1992

0;

AAQ30432;

Page 227

us09904568-1.rng

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vitro or in vivo; (viii) constructing genes and vectors, particularly for development of pharmaceuticals; (ix) developing diagnostic kits and other systems for genotyping; and (x) developing in vivo and in vitro test systems for expressing individual forms of the MSH6 gene, e.g. for studying pathophysiology of disease or processes in which MSH6 is involved, and for drug development and testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNAc comprising a promoter P and an L1 cassette sequence having a core retrotransposon element, useful for random insertion of a heterologous or homologous DNA sequence into a cell genome and for correcting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to DNA for a promoter and an Il cassette sequence having a core retrotransposon element. The invention is useful for random insertion of a heterologous or homologous DNA sequence into a cell genome, and for correction of a genetic defect in the cell into which the insertion is made. Genetic defects which may be corrected includes cystic fibrosis, mutations in the dystrophin gene, genetic defects associated with blood clotting and
                                                                                                                                                                               Gaps
                                                                                                                                                                              ;
                                                                                                                                          Score 17; DB 1; Length 22; 
Pred. No. 2.4e+02; 
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retrotransposon; genetic defect; cystic fibrosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 17; DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boeke JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 22 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                 Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 other;
                                                                                                                                   1.5%; bcc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          L1 cleavage site related sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 14; 87pp; English
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96US-0749805.
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Query Match
Beet Local Similarity 100.00
Beat 17; Conservative
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(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                              22 AAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                            AAF17413 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other genetic defects.
                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-060015/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic defects -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L6-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2001
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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tummours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "o-xyloso dimer synthon linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Froehler B, Krawczyk S, Matteucci MD, Milligan J;
                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
|2..23
                                                                                                                                                                                                                 "mod_base= OTHER
'note= "OTHER= N4 N4 ethanocytosine'
                                                                                                                                                                                                                                                                                                                   inverted_polarity_region
                                                                                                                                                                                                                                                                                                        *tag= c
label= inverted_pola
note= "see comments"
                                                                                                                                                                             Location/Qualifiers
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91US-0686546.
91US-0686547.
91US-0766733.
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                                                                                                                                                                                                    '*tag= a
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                                                                                                                                                                             Key
modified_base
                                                                                                                                                                                                                                           modified base
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                                                                                                                                                                                                                                                                                            misc feature
                                                                                                                                                                                                                                                                                                                                               misc_feature
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08-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1991;
17-APR-1991;
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Gaps

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Indels

100.0%; Preq. ...

1084 AAAAAAAAAAAAA 1100

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1 AAAAAAAAAAAAAA 17

Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 other;

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1084 AAAAAAAAAAAAAA 1100

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22 AAAAAAAAAAAAAAA 6

AAQ45360 standard; DNA; 23 BP.

RESULT 524 AAQ45360,

and the same

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AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo; removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect Abs, in which case the ligand is an oligo-labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary olgi is AAQ75024 which can be covalently attached by the 5'-terminat to the N- or C-terminal of a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 23; 100.0%; Pred. No. 2.5e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 19 A; 4 C; 0 G; 0 U; 0 other;
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                                                                                                                                                                           Synthetic oligo; solid phase immunoassay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 AAAAAAAAAAAAA 1100
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    AAQ75028 standard; DNA; 23
                                                                              (updated)
(first entry)
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(first entry)
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mes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-006819/01.
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                                                                                                                                                                                                                                                                                                                                  13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                      13-MAY-1993;
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                                                                                                                                                                                                                                                                                          24-NOV-1994.
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03-AUG-1995
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                                                                            25-MAR-2003
03-AUG-1995
                                                                                                                                      LCR oligo 2
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                                                                                                                                                                                                                 Synthetic.
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                                          AAQ75028;
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                                                                                                                                                                                                                                   Gaps
(nucleotides have the 3'positions of xylose sugars linked via the o-xylene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for diagnosis and treatment of diseases associated with abnormal PTP-ID levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA primer is used in the PCR-based amplification of protein-tyrosine-phosphatase-1B cDNA. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 1.5%; Score 17; DB 1; Length 23; Local Similarity 100.0%; Pred. No. 2.5e+02; No. 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         Query Match
1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein-tyrosine-phosphatase; enzyme; disease diagnosis;
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Human protein-tyrosine-phosphatase-1D cDNA primer.

ONA primer; ss.

Synthetic.

WO9408017-A1.

(updated)
(first entry)

25-MAR-2003 09-OCT-1994

(PLAC) MAX PLANCK GES FORRDERUNG WISSENSCHAFTEN.

Ullrich A, Vogel W; WPI; 1994-135583/16.

93US-0018129 92US-0956315

93WO-EP02728

06-OCT-1993; 06-OCT-1992; 16-FEB-1993;

peptides. t. The

0

Gaps

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RESULT 525 AAQ75028

Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;

Query Match

Best Loca Matches

1084 AAAAAAAAAAAA 1100

AAAAAAAAAAAAA 7

23

Disclosure; Page 48; 99pp; English

The self list of the

(SHKJ) RES DEV CORP JAPAN.

Kato K;

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                                                                                                                                                                                                                                                                                              AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo; removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect ABs, in which case the ligand is an oligo-labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary olgi is AAQ75024 which can be covalently attached by the 5'-terminus to the N- or C-terminal of a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                   Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer #1 for tissue or cell derived RNA.
                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "hydroxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                      Example; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAAA 1100
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95JP-0184006
                                           94WO-US05407
                                                                            93US-0061694
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                                                                                                                                          Khudyakov YE;
                                                                                                                                                                         WPI; 1995-006819/01.
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                                                                            13-MAY-1993;
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20-JUL-1995;
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               24-NOV-1994
                                                                                                                                          Fields HA,
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transcription of tissue or cell derived mRNA, in the method of the transcription of tissue or cell derived mRNA, in the method of the invention is a molecular indexing method, and comprises digesting the cDNA amplified by these sequences with a class IIS restriction enzyme. Each resultant CDNA fragment is then lighted to a biotinylated adaptor (selected from a pool of 64 adaptors cheesive to all possible overhangs), and digesting the products with two further class IIS restriction enzymes. These steps are repeated (but therrent class IIS restriction enzymes. These steps are repeated (but therrent class IIS restriction enzymes. These steps are repeated (but therrent class IIS restriction enzymes. These steps are repeated (but therrent class IIS restriction samples are then recovered using streptavidin-coated paramagnetic beads, removing the strand complementary to an adaptor-primer. The adaptor primer and an anchored complementary to an adaptor-primer. The adaptor primer and include an analysis samples. The amplified products are separated, and the sizes of the fragments obtained is recorded. The method can be used for the cDNA samples. The adaptore is a second as a cancers or viral infections, for the search and isolation of the genes of physiologically active substances that are potential pharmaceuticals, or causative genes of hereditary diseases, as well as for the isolation of genes for improving agricultural products. Using this method, it is possible to classify (index) DNA into groups in a short period of time without duplication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                           Molecular indexing of DNA - using restriction enzymes, PCR amplification and electrophoresis to analyse DNA fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.5%; Score 17; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT-PCR Primer for aromatic acyl transferase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
                                                                                                                                                                                                        Claim 3; Page 14; 20pp; English.
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AAT37316 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 TAAAAAAAAAAAA 7
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95JP-0196915.
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                                                                                                   WPI; 1996-435619/44
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17-FEB-1995;
29-JUN-1995;
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(SUNR) SUNTORY LID

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Kusumi T, Mizutani M;
T, Fujiwara H, Fukui Y,
Tanaka Y, Yonekura K;
                       Nakao M,
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WPI; 1996-393401/39

DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers

Example 2; Page 21; 94pp; Japanese.

Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. This primer was used to reverse transcribe aromatic acyl transferase RNA to produce a cDNA ready for cloning into expression vectors

Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;

Gaps .. 0 Query Match
1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

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1084 AAAAAAAAAAAAAA 1100 23 AAAAAAAAAAAAAA

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AAV61555 standard; DNA; 23 BP. AAV61555,

(first entry) 08-DEC-1998 Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.

Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver; kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression; internal standard; calibration curve; ss.

Synthetic. Mus sp.

EP870842-A2

14-OCT-1998

98EP-0302726 17-APR-1998;

(NISC-) JAPAN SCI & TECHNOLOGY CORP. 97JP-0088495 07-APR-1997;

Kato K;

WPI; 1998-523164/45.

Determination of gene expression levels - using combinations different cDNA samples tagged with different PCR adaptors

Example 2; Page 9; 22pp; English.

The present sequence represents a primer which was used to synthesise Apolipoprotein DDNA in a RT-PCR reaction. This primer as well as primers AAV61554 and AAV61556 were added to both mouse liver-derived and mouse kidney-derived total RNA to generate single-stranded cDNA. These

ö primers were used in the method of the invention to determine the amount ratio between a cDNA coding for mouse liver-derived Apoliopprotein and a cDNA that codes for the mouse kidney-derived Apoliopprotein by using Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene expression to be quantitatively determined, and because internal standards are not required to prepare a calibration curve, it is a quicker and less laborious process. Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA. Primer, PCR; amplification; RT-PCR; quantitate; amount ratio; liver; kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression; internal standard; calibration curve; ss. Gaps ٥Ę 0; Determination of gene expression levels - using combinations different cDNA samples tagged with different PCR adaptors Query Match
1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other; (NISC-) JAPAN SCI & TECHNOLOGY CORP. Example 2; Page 9; 22pp; English. 1083 TAAAAAAAAAAAA 1099 BP. 7 98EP-0302726 97JP-0088495 23 TABABABABABABA AAV61556 standard; DNA; 23 (first entry) WPI; 1998-523164/45. 07-APR-1998; 07-APR-1997; 08-DEC-1998 14-0CT-1998. EP870842-A2 Synthetic. Mus sp. RESULT 530 AAV61556/c 8888888833ò

0 The present sequence represents a primer which was used to synthesise Apolioporotein CDNA in a RT-PCR reaction. This primer as well as primers AAV61554 and AAV61555 were added to both mouse liver-derived and mouse kidney-derived total RNA to generate single-stranded CDNA. These primers were used in the method of the invention to determine the amount ratio between a CDNA coding for mouse liver-derived Apolioporotein and a CDNA that codes for the mouse kidney-derived Apolioporotein and a Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene expression to be quantitatively determined, and because internal standards are not required to prepare a calibration curve, it is a quicker and less laborious process. Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Gaps .. Query Match 1.5%; Score 17; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels

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29-MAR-1999;
                                                                          misc_RNA
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                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a primer which was used to synthesise Apolipoprotein CDNA in a RT-PCR reaction. This primer as well as primers AAV61555 and AAV61556 were added to both mouse liver-derived and mouse kidney-derived total RNA to generate single-stranded CDNA. These primers were used in the method of the invention to determine the amount ratio between a CDNA coding for mouse liver-derived Apolipoprotein and a Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene expression to be quantitatively determined, and because internal standards are not required to prepare a calibration curve, it is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage of nucleic acids from solid supports assay oligonucleotide #1.
                                                                                                                              Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver; apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression; internal standard; calibration curve; ss.
                                                                                                                                                                                                                                                                                                                                                          Determination of gene expression levels - using combinations of different cDNA samples tagged with different PCR adaptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quicker and less laborious process.
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                    ТАДАДАДАДАДАДАДАД
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                                                                      AAV61554 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local S:
Matches 17
                                                                                                                                                                                         Synthetic.
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                                                                                          AAV61554;
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                                                            AAV61554/c
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The present invention is concerned with the cleavage of nucleic acids from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, cDNA and template preparation, DNA-based assays, mutagenesis procedures, nucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used in assays to demonstrate the methods of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detaching nucleic acid molecule comprising unconventional nucleotide incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional
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Nucleic acid cleavage; solid support; DNA-RNA hybrid;
affinity chromatography; sequencing; mutagenesis; DNA preparation;
nucleic acid purification; ss.
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                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                        Synthetic
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Seguence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Thu Jan

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Detaching nucleic acid molecule comprising unconventional nucleotide incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional
                                                                                                                                                                                                                                                                                         Example 1; Page 32; 47pp; English.
(GOLD/) GOLDSBOROUGH A.
                                                               WPI; 2000-664908/64
                                                                                                                                                                                                                                 nucleotide
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The present invention is concerned with the cleavage of nucleic acids from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, CDNA and template preparation, DNA-based assays, mutagenesis procedures, nucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used in assays to demonstrate the methods of the invention. 1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Sequence 23 BP; 0 A; 0 C; 0 G; 23 U; 0 other; 17; Conservative Best_Local Similarity Matches 17; Conserv Query Match ö

1084 AAAAAAAAAAAAAA 1100 7 AAAAAAAAAAAAAAA 23 g

AAA08407 standard; DNA; 23 RESULT 53

BP.

13-JUL-2000 AAA08407;

(first entry)

Oligonucleotide primer SEQ ID NO:1.

Detection, primer, adapter; probe, hybridisation, gene cluster; fractionation; ss.

Synthetic.

JP2000055914-A.

25-FEB-2000

98JP-0228944 13-AUG-1998; (TAIS) TAISHO PHARM CO LTD

98JP-0228944.

13-AUG-1998;

WPI; 2000-368733/32.

detection method involves hybridizing probe opposite to objective out of fractional gene cluster Gene gene

Example 1; Page 9; 11pp; Japanese.

The present invention describes a gene detection method which comprises fractionating using a probe opposite to the objective gene which is hybridised out of fractioned gene cluster. The objective gene detected belongs to the group of objective genes contained in the sample. The method is used for gene detection by fractionation of cDNA by molecular index method using specific primer. It provides high detection sensitivity of objective gene. AAA08407 to AAA08414 represent oligonucleotides used in the exemplification of the present invention.

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                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid molecule encoding amino acid sequence capable of forming cyclic structure, for generating transgenic plants capable of producing cyclic knotted protein and resistant to pathogens such as
                 Gaps
                                                                                                                                                                  Kalata B2; transgenic plant; cotton; calcium channel binding; pain; stroke; C5a binding; antiinflammatory; PCR primer; ss.
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0
                                                                                                                                                 PCR primer for DNA encoding Kalata B1 polypeptide fragments.
Length 23;
                 0; Indels
Score 17; DB 1; L
Pred. No. 2.5e+02;
        Local Similarity 100.0%; Pred. No. 2.5 les 17; Conservative 0; Mismatches
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AAF85497 standard; DNA; 23
                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                               (UYLA-) UNIV QUEENSLAND.
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25-NOV-1999;
                                                                                                                                    23-JUL-2001
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 Query Match
                                                                                 RESULT 535
                    Matches
                                                                                         AAF85497,
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Gaps

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Length 23; 0; Indels Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

infestation

protecting plants such as crop plants from pest and/or pathogen

PCR primers AAF85495-97 were used to amplify a DNA fragment encoding ralata B1. Kalata B1 is a macrocyclic peptide with diverse biological activities. The Kalata B1 polymucleotide represents a nucleic acid molecule of the invention. The specification describes nucleic acid molecules which encode an amino acid sequence which is capable of being cyclised within a cell or a membrane of a cell to form a cyclic backbone. The amino acid sequence comparises sufficient disulfide bonds to confer a stabilized folded structure on the three-dimensional structure of the backbone. The nucleic acid molecules of the invention are useful for broducing transgenic genetically modified food or non-food crop plants, producing transgenic genetically modified food or non-food crop plants, producing transgenic genetically modified food or non-food crop plants, introduce modulating activity, for modulating activity of calcium channel binding is useful in treatment of pain or stroke and CSa binding activity useful as an antibiliflammatory agent. The nucleic acid molecules are useful in the generation of molecules having animal or plant therapeutic properties as well as in a range of diagnostic, industrial adjuntational agricultural including horicultural applications and for an adjunctural including horicultural applications and for

Example 10; Fig 1B; 112pp; English.

Length 23; DB 1; 1.5%; Score 17;

Query Match

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us09904568-1.rng

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Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of
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                                                                                                                                                                                                                                                                                                                                                          (AGIL-) AGILENT TECHNOLOGIES INC.
                                                                                                                                                                                                                                             10-SEP-2001; 2001EP-0307665
                                                                                                                                                                                                                                                                                                    11-SEP-2000; 2000US-0659173
                            88.
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                         Molecular array; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calibration probes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastric acid disturbance; gastric reflux; gastritis; dyspepsia; stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense; DNA-RNA hybrid; ss.
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                               Mismatches
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     100.0%;
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Matches 17; Conservative
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Matches
                                                                                                                                                                                                                               RESULT 536
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ð g BXHXHXB

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The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from a molecular array. The present sequence is poly (A) normalisation probe used in calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5%; Score 17; DB 1; Length 23; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #48 for assaying nucleic acids.
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03-AUG-2000; 2000JP-0236115.
26-SEP-2000; 2000JP-0292483.
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Best Local Similarity 100.8
Matches 17; Conservative
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(KANK-) KANKYO ENG CO LTD
                            RESULT 539
                             ABA99682,
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                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to nucleic acid probes, which are useful for assaying nucleic acids by hybridising with a target nucleic acid, in which a single-stranded oligonucleotide is labelled with a fluorescent substance and a quencher in a manner that the fluorescence intensity of the hybridisation reaction system is increased after completion of the hybridisation but no stem loop structure is formed. The probes are useful for assaying nucleic acids and their polymorphism and mutation, particularly useful for e.g. analytical applications, disease diagnosis and microbial identification. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for testing the effect of a substance as a preventive or treating agent for osteoporosis or arthro-rheumatism. This sequence represents a PCR primer used in the amplification of a gene encoding a protein associated with osteoporosis or arthro-rheumatism which is described in the disclosure of the
                                                                                                                                                                  Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine osteoporosis/arthro-rheumatism associated gene PCR primer DAPA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventing or treating an agent for osteoporosis or arthro-rheumatism
Yamada K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osteoporosis; murine; treatment; arthro-rheumatism; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Kurata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.5%; Score 17; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels
Torimura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 other;
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Kamagata Y,
                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig. 3; 152pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAAAA 1100
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       Kanagawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-288360/33.
                                                                                                       MPI; 2002-195876/25.
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       Kurane R,
Yokomaku T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transfers a sugar to the 3' position of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the genes and proteins of glycosyltransferases from Gentiana triflora, Senesio cruentus and Clitoria ternatea. The protein transfers a sugar to the 3' position canthocyanin, and can be used for changing the colour of flowers. The present sequence is a PCR primer used to isolate glycosyltransferase coding sequences of the invention.
                                                         Gaps
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                                Length 23;
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                                1.5%; Score 17; DB 1; Le
.00.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;
       Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA probe used in fingerprinting technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                       100.0%; Pred. No. -
                                                                                                                                                                                                                                              Glycosyltransferase genes PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New gene encoding protein that transfe
anthocyanin for changing flower color
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 13; 50pp; Japanese.
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                                                                                 1083 TAAAAAAAAAAAAA 1099
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                                                                                                                                                                       BP.
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                                                                                                          23 TAAAAAAAAAAAAAAA
                                                                                                                                                                       ABA97431 standard; DNA; 23
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                                                          Conservative
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                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                      21-MAR-2002
                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001
                                                          17;
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AAT6861
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Vematsu

Okano K,

96EP-0118921 95JP-0311949

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The present sequence is a DNA probe used in a novel method of analysis or assay for nucleotides, which comprises: (i) digesting DNA with a DNA fragments obtained around the 3' termini with a DNA probe and extending the DNA probe by a complementary strand synthesis to fractionate the DNA fragments into groups; and (iii) measuring lengths of the DNA fragments which belong to the groups, or length of the extended DNA probe, and using the lengths obtained for the fragments around the 3' termini as fingerprints. Where polyA is present presence of recognition sequence GGG is critical for clarifying the terminal site, this is because the length of polyA cannot be controlled. The method is useful for assaying long DNA fragments and for assaying long DNA sequences.
probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
                                                                                                                                                                                                                                                 Nucleic acid assay methods - based on restriction fragment length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a synthetic oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 2 other;
                                                                                                                                                                                                                                                                                          Example 1; Page 7; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid immobilisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH43079 standard; DNA; 24 BP
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                                                                                                                                                                   (HITA ) HITACHI LTD.
                                                                                                                                                                                                                        WPI; 1997-300347/28
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                                                                                                                                                                                                                                                                  determination
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                                                                                                               26-NOV-1996;
                                                                                                                                           30-NOV-1995;
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                                                                                   11-JUN-1997.
                                                          EP778351-A2
                                                                                                                                                                                              Kambara H,
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                               Synthetic.
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Best Local S
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damaging
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                                                                                                                       The specification describes a support for immobilizing nucleotides which contributes to the efficient clarification of DNA without damagin the terminal parts of the DNA. The support is a chemically treated modified substrate on which oligonucleotides with restriction enzyme cleavage sites are immobilised. The support is useful for immobilizing nucleic acids such as DNA. The present sequence represents a synthetic oligonucleotide used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immuno disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                             Length 24;
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                                                                                                                                                                                                                                                                                                             1.5%; Score 17; DB 1; Li
100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
                                                                                                                                                                                                                                                                          Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.66
Matches 17; Conservative 0; Mismatches
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                                                  Support for immobilizing nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 12; 38pp; Chinese.
                                                                                        Example 1; Page 8; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                         1084 AAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                               23 AAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH24266 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                 WPI; 2001-488794/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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AAH24266/C
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1.5%; Score 17; DB 1; Length 24; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels

17; Conservative

Similarity

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19

(first entry)

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Takahashi K;

Okamura H, Takagi K,

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ABK86172;

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activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reaction or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH24265-AAH34266 represent reverse transcription-PCR (RT-PCR) primers used in an exemplification of the invention to isolate human phosphatase 79 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and genetic engineering fields. Sequences ABQ79871-881 represent PCR primers used in the method of the invention.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carrying out a thermal cycle of polymerase chain reaction (PCR) by using a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain reaction; thermal cycle; immobilisation; genetic engineering; PCR; primer; ss.
                                                                                                                                                    Length 24;
                                                                                                                                                                                   0; Indels
                                                                                                                                                    1.5%; Score 17; DB 1; Le
.00.0%; Pred. No. 2.6e+02;
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                                                                                                                     Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 other;
                                                                                                                                                                100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a PCR primer #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examples; Page 10; 13pp; Japanese
                                                                                                                                                                                                                      1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                     ABQ79878 standard; DNA; 24 BP.
                                                                                                                                                                                                                                         27-DEC-2000; 2000JP-0399573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-2000; 2000JP-0399573
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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(TAKA/) TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 100.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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ABQ79878/c
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The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having a specific oligo-dT primer sequence, where the identimer comprises a cetectable marker at its 5' and. The system is useful for identifying any cor all genes expressed in a given in vivo or in vitro RNA sample, as well genes expressed in a given in vivo or in vitro RNA sample, as well cet size, for supporting discovery of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing cortions in the needed to enable the assay; (b) provides immediate sequence information in addition to information corlone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information level and mRNA identification in neassay; (c) generates CDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology cortexing significant genomic sequence in formation. The present corganisms lacking significant genomic sequence in formation. The present subsequence represents an oligo dT primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                         Oligo dT primer #4 used in method to study gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 24; 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                 Oligo dT primer; gene expression analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.5%; Score 17; DB Local Similarity 100.0%; Pred. No. 2.6 nes 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Nagel AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 15; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN85073 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOMIC SOLUTIONS INC
                                                                                                                                                                                                                                                                              01-NOV-2001; 2001WO-US45401.
                                                                                                                                                                                                                                                                                                                      01-NOV-2000; 2000US-244933P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                 Kane MD, Dombkowski AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-508123/54.
                                                                                                                                                                                                  WO200236828-A2,
                                       24-SEP-2002
                                                                                                                                                                                                                                      10-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN85073;
                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN85073/c
ID ABN8:
XX
AC ABN8:
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Gaps

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1084 AAAAAAAAAAAAA 1100

Local

Matches

AAAAAAAAAAAAAAA

23

ABK86172/c ID ABK86172 standard; DNA; 24 BP. XX

RESULT 545

05-SEP-2002 (first entry)

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The present invention relates to human S4 ribosomal protein 13.97 (see ABB83379). The ribosomal protein and its coding sequence are useful for treating malignant tumours, hemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primar, which was used in an example from the invention.
                                           Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T7T18Apad_P512-24-0001 probe for calibration of molecular array data.
                                                                                                                                                                                                                                                                                                        Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide, useful for treating malignant tumor, inflammation, hemopathy, human immunodeficiency virus infection, immunological
                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 16 (Disclosure); 33pp; Chinese.
                    Human S4 ribosomal protein 13.97 PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;
                                                                                                                                                                                                                                (SHAN-) SHANGHAI BIODOOR GENE DEV CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGIL-) AGILENT TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD33505 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-2000; 2000US-0659173
                                                                                                                                                                               07-JUL-2000; 2000CN-0117077
                                                                                                                                                                                                        07-JUL-2000; 2000CN-0117077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular array; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wobler PK, Delenstarr GC;
                                                                                                                                                                                                                                                                                                                                                   disease and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                   WPI; 2002-292916/34.
                                                              HIV intection, PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1186673-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-2002
                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-MAR-2002
                                                                                                                              CN1333268-A
                                                                                                                                                       30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD33505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                                                                                                                                                          Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD33505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Gaps

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0; Indels

1.5%; Score 17; DB 1; Length 24; 100.0%; Pred. No. 2.6e+02;

100.0%; Preα.

17; Conservative

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24 AAAAAAAAAAAAAAA

(first entry)

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The invention relates to human gonadotropin-releasing hormone 10 (AAAM49158) and to nucleic acids encoding it (ABL55128). The protein has a molecular weight of 10 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Gonadotropin-releasing hormone 10 can be used in the treatment of a variety of diseases such as cancer and HIV (human
                                                                                                                                                                            The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating different scanned from different arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide encoding it -
                                               Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gonadotropin-releasing hormone 10; recombinant production; cancer; HIV infection; human immunodeficiency virus; gene therapy; cytostatic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.5%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 17 (Disclosure); 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                            Seguence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                              Disclosure; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2000; 2000CN-0116266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-2000; 2000CN-0116266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL55130 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-196660/26.
               WPI; 2002-282886/33
                                                                                           target molecules, a
calibration probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1325900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL55130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Мао У,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 548
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immunodeficiency virus) infection. Sequences ABL55129-ABL55130 represent reverse transcription-PCR (RT-PCR) primers used in an exemplification of the invention to isolate human gonadotropin-releasing hormone 10 cDNA.
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Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 other;

Gaps ۰, Length 24; 0; Indels Score 17; DB 1; Le Pred. No. 2.6e+02; Query Match 1.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 17; Conservative 0; Mismatches

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> ₹ QC

RESULT 549

ABX79809/c ID ABX79809 standard; cDNA; 24 BP ABX79809; polymorphic DNA repeat polynucleotide #134.

17-APR-2003 (first entry)

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POWPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

Homo sapiens

US6472154-B1

29-OCT-2002

99US-0475947. 31-DEC-1999; 99US-0475947.

31-DEC-1999;

(TEXA) UNIV TEXAS SYSTEM.

Fondon JW;

Minna JD,

Wren JD,

Garner HR,

WPI; 2003-208818/20.

Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability -

Examples; Column 579; 588pp; English.

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, poNROUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs.

0;

Gaps

;

Length 20; Indels

1.5%; Score 16.8; DB 1; ilarity 90.0%; Pred. No. 2.3e+02; Conservative 0; Mismatches

Local Similarity ses 18; Conserv

Matches

à dd

Query Match

996 AGTCTGAGGCTGGAGATGG 1015

AGGCTGAGGCAGGAGAATGG 20

RESULT 551 AAS29488

Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;

soft

Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ37473-Z33738 represent human mdm2 phosphorothioate oligonucleotides. AAZ37411, AAZ37472, AAZ37740 and AAZ37741 are used in the exemplification of the present invention. The present invention describes novel nucleotide antisense compounds, targetted to the 5' untranslated, translation termination codon, or 3' untranslated region of a nucleic acid encoding human mdm2, that modulates expression of human mdm2. The oligonucleotides mediate their effect by antisense inhibition of hyperproliferative gene expression. The antisense compound is used to treat an animal having a disease or condition associated particularly a hyperproliferative condition, more particularly a hyperproliferative condition, more particularly cancer, especially of the blood, brain, breast, lung or soft tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compounds used to treat eg. hyperproliferative conditions
                                   Gaps
                                                                                                                                                                                                                                                                                                                      Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;
cancer; antisense; modulation; oligonucleotide; expression;
inhibition; hyperproliferation; blood cancer; brain cancer;
breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
                                   .
0
1.5%; Score 17; DB 1; Length 24;
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowsert LM
                                                                                                                                                                                                                                                                                       Human mdm2 phosphorothioate oligodeoxynucleotide #249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 54; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham MJ,
                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis; restenosis; ss
                                                                        1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                          BP.
                                                                                                      23 AAAAAAAAAAAAAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US06702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0048810
                                                                                                                                                                                          AAZ37719 standard; DNA; 20
                                                                                                                                                                                                                                                             (first entry)
       Query Match 1.5'
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nero P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610754/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09949065-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miraglia LJ,
                                                                                                                                                                                                                                                             07-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                             AAZ37719;
                                                                                                                                                                             AAZ37719
                                                                                                                                                             RESULT
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AAS29488 standard; DNA; 20

(first entry)

us09904568-1.rng

Page 239

o;

Gaps

0

Indels

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0; Mismatches

MIRA/) MIRAGLIA L J.

NERO P. GRAHAM M J.

(NERO/) GRAH/)

99US-0280805.

/note= "OTHER= All phosphorothioate linkages, additionally bases 1-6 and bases 15-20 are 2'-0-methoxyethyl bases, and bases 7-14 are deoxymucleotides"

ocation/Qualifiers

/*tag= a /mod_base= OTHER

Score 16.8; DB 1; Length 20; Pred. No. 2.3e+02; 1.5%; Query Match Best Local Similarity

Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;

the present invention.

. 0

The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the PAP28 collagragion. The BAP28 polypeptides can be expressed by standard recombinant methodology BAP28 polymerlectides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from c susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. Sequences AAP83934-963 represent primers for the BAP28 gene and PCTA-1 gene (the coding strand of BAP28). New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays -Gaps . 0 tumour; cancer; diagnostic; genetic analysis; Length 20; Indels Chumakov I, Cohen-Akenine A; BAP28 gene fragment amplifying primer BAP28polyTcourt. Query Match
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other; Examples; Page 347; 349pp; English. 1080 TATTAAAAAAAAAAA 1099 996 AGTCTGAGGCTGGAGAATGG 1015 TATACAAAAAAAAAAAAA 1 AAF80873 standard; DNA; 20 BP. 1 AGGCTGAGGCAGGAGATGG AAF83959 standard; DNA; 20 BP. 23-JUN-2000; 2000WO-IB01183. 25-JUN-1999; 99US-0141323 18-JAN-2000; 2000US-0176880 (first entry) Bougueleret L, 18; Conservative BAP28; prostate; tumour PCTA-1; PCR primer; ss. WPI; 2001-367032/38. (GEST) GENSET. WO200100669-A2 Homo sapiens. 04-JAN-2001. 06-AUG-2001 20 AAF80873; Barry C, AAF83959; RESULT 553 AAF80873
ID AAF8
XX
AC AAFE Matches RESULT 55 AAF83959/ à 셤 ò g The present invention relates to antisense compounds, 8-30 nucleobases in length targeted to the 5' untranslated region, translation termination codon region, 3' untranslated region, translation translation at expisers of a nucleic acid encoding human mdm2, where the antisense compound modulates the expression of human mdm2. The antisense compound modulates the expression of human mdm2. The manisense oligonuclectides of the invention are useful for encoding human mdm2 and for inhibiting the expression of human mdm2. They may be used for treating an animal having a disease or condition associated with amplification of mdm2 gene or overexpression of mdm2. They may be used for treating an animal having a disease or condition associated with a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or restenosis, tunnours, colorectal carcinoma and chronic myelogenous cettemosis, tunnours, colorectal carcinoma and chronic myelogenous compound reduces hyperproliferation of human cells. The method, which involves the use of the antisense compound, is also useful for detecting the role of mdm2 expression in various cell functions and physiological processes and useful in both clinical research and diagnostic tools.

AAS29244-AAS39507 represent the human mdm2 antisense oligonucleotides

Cowsert LM;

Graham MJ, Monia BP,

Nero P,

MONIA B P. COWSERT L M.

(MONI/)

(first entry)

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Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
                                                                                                                                                                                                                                                                                                                                   nucleic acid molecule encoding human mdm-2 useful for modulating the expression of human mdm-2 and reducing hyperproliferation of human
                                                                                                                                                                                                                                                                                                                         Novel antisense compound 8-30 nucleobases in length targeted to a
                                                                                                                                                                                                                                                                                                                                                                                                                                      mucleobases in length targeted to nucleobases 1-308 of the 5' untranslated region, 1776-1806 of the translation termination codon region or 1818-2370 of the 3' untranslated region of a nucleic acid molecule encoding human mdm.2. The invention is useful for reducing hyperproliferation of human cells, modulating the expression of mdm2 in human cells or tissues or in vitro. The hyperproliferative disorder includes cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to an antisense compound 8-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine SAC1 gene-specific oligonucleotide PCR primer #400.
                                                     Antisense; mdm2; hyperproliferation; cancer; psoriagis; ss
                           Human mdm2 phosphorothioate oligonucleotide #247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Column 31; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   996 AGTCTGAGGCTGGAGAATGG 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2001; 2001WO-US13387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein replacement therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS97833 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                             WPI; 2001-190948/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200183749-A2.
                                                                                                                                                                                                        26-MAR-1998;
                                                                                                                                                                                                                                                                 Miraglia LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-2002
                                                                                       Homo sapiens
                                                                                                                  JS6184212-B1
                                                                                                                                                                            26-MAR-1999;
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02-MAY-2001
                                                                                                                                               06-FEB-2001
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The invention relates to an isolated polypeptide, comprising a variant form of mouse or human SAC1 polypeptide. The variant form is associated with altered preference for carbohydrates, other sweeteners or ethanol. The polypeptide and its associated DNA sequence can be produced by recombinant techniques and is useful for preventing obesity, diabetes or alcoholism associated with SAC1 expression. The sequences are useful in screening for drugs and sweeteners. Recombinant cell lines and transgenic embryos may be used in screening for and identifying agents that induce or repress function of SAC1. Predisposition to diabetes, obesity or alcoholism can be ascertained by testing any fluid or tissue of a human (such as blood, pancreas or tongue) for sequence variations of the SAC1 locus may indicate a predisposition to diabetes, obesity and/or alcoholism and may provide a diagnostic mark. The polymuclectide can be detected in a biological sample by contacting the DNA with a probe to form a hybridisation complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
protein replacement therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which is then detected. The sequences represent cDNA encoding human and mouse SAC1 polypeptides and PCR primers specific for the SCA1 genes.
                                                                                                                            Li X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                     mouse or human
                                                                                                                                                                                                                   Novel isolated polypeptide comprising variant form of mouse or hu SACI polypeptide, and is associated with altered preference for carbohydrates or other sweeteners, useful for preventing obesity,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5%; Score 16.8; DB 1; Length 2 90.0%; Pred. No. 2.38+02; ive 0; Mismatches 2; Indels
                                                                                                                            De Jong PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 7 A; 0 C; 10 G; 3 T; 0 other;
                                                                                                                              Chatterjee A,
Tordoff MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000 TGAGGCTGGAGAATGGGAAG 1019
                                                                                                                                                                                                                                                                                                                 Claim 14; Page 89; 239pp; English.
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                                                                       (WARN ) WARNER LAMBERT CO. (MONE-) MONELL CHEM SENSES CENT.
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ID AAS97860 standard; DNA; 20 BP.
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28-JUL-2000; 2000US-221419P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2001; 2001WO-US13387
                                                                                                                              Beauchamp GK,
I DR, Ross D,
28-APR-2000; 2000US-200794P.
28-JUL-2000; 2000US-221419P.
10-NOV-2000; 2000US-247443P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                            diabetes, alcoholism
                                                                                                                              Bachmanov AA, Beauc
Ohmen JD, Reed DR,
                                                                                                                                                                                    WPI; 2002-075162/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS97860;
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Gaps

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2; Indels

Score 16.8; DB 1; Pred. No. 2.3e+02; 0; Mismatches 2;

0;

1.5%;

AGGCTGAGGCAGGAGAATGG 20

BP

(first entry)

Length 20;

Cowsert LM

Monia BP,

Graham MJ,

Nero P,

99US-0280805 98US-0048810 ; 0

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diabetes, alcoholism
                                                                                               Best Local Similarity
                   WPI; 2002-075162/10.
                                                                                                                                                                            19-MAR-1998;
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                                                                                                                                                                  VO9841648-A2
                                                                                                                                                                       24-SEP-1998
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                                                                                                                            AAZ26500;
                                                                                            Query Match
                                                                                                                  RESULT 556
                                                                                                                                                             Ношо
                                                                                                 Matches
                                                                                                                     AAZ26500
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potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (Loh) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders,
                                                                                                                                                     Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plague, dysplastic lesions, endometriosis or graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; single nucleotide polymorphic; SNP; forensic science; paternity testing; phenotypic trait; genetic mapping; animal breeding; plant breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycybric kidney disease, and graft versus host disease. The method can also be used tremove malignant cells from bone marrow transplants. AAZ25812-Z26825
                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for identifying an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent human polymorphic sites described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 1.5%; Score 16.8; DB 1; Length 21; 1 Similarity 90.0%; Pred. No. 2.4e+02; 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polymorphic oligonucleotide Y12855 fragment #5.
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                                                                                                                                                                                                                                                                       Disclosure; Figure 7; 605pp; English
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                                                     Stanton VP;
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(VARI-) VARIAGENICS INC
                                                     Ledley FD,
                                                                                                           WPI; 1998-521232/44.
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Matches 18; Conserv
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                                                     Housman D,
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The polypeptide and its associated DNA sequence can be produced by recombinant techniques and is useful for preventing obesity, diabetes or alcoholism associated with SAC1 expression. The sequences are useful in screening for drugs and sweeteners. Recombinant cell lines and transgence embryos may be used in screening for and identifying agents that induce or repress function of SAC1. Predisposition to diabetes, obesity or alcoholism can be ascertained by testing any fluid or tissue of a human (such as blood, pancreas or tongue) for sequence variations of the SAC1 of gene. A sequence variation of the SAC1 locus may indicate a predisposition to diabetes, obesity and/or alcoholism and may provide a diagnostic mark. The polymuclectide can be detected in a biological sample by contacting the DNA with a probe to form a hybridisation complex which is then detected. The sequence represent cDNA encoding human and mouse SAC1 polypeptides and PCR primers specific for the SCA1 genes.
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                                                                                                                                  Li X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                 Novel isolated polypeptide comprising variant form of mouse or human SAC1 polypeptide, and is associated with altered preference for carbohydrates or other sweeteners, useful for preventing obesity,
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Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                  De Jong PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 10 C; 0 G; 7 T; 0 other;
                                                                                                                               Chatterjee A,
Tordoff MG;
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 90; 239pp; English.
                                                (WARN ) WARNER LAMBERT CO. (MONE-) MONELL CHEM SENSES CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%;
                                                                                                                               Bachmanov AA, Beauchamp GK,
Ohmen JD, Reed DR, Ross D,
10-NOV-2000; 2000US-247443P.
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LO-NOV-2000; 2000WO-US30766.

17-MAY-2001

99US-0164596.

10-NOV-1999;

97US-0041057.

(GLAX) GLAXO GROUP LTD

The present invention relates to human oligonucleotides comprising a single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present sequence is one such oligonucleotide. The oligonucleotides can be used in forensics, paternity testing, correlation of polymorphisms with phenotypic traits, genetic mapping of phenotypic traits and marker assisted breeding of animals and crop plants. New polymorphic sites derived from the human genome are useful to determine sites correlating with phenotypic traits, particularly disease, and also in forensics and paternity testing Sequence 21 BP; 3 A; 9 C; 4 G; 5 T; 0 other; Thomas D; Claim 27; Page 7; 43pp; English Chen J, Patil N, (AFFY-) AFFYMETRIX INC WPI; 2001-335945/35 Au Κ,

1.5%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 2.4e+02; ive 0; Mismatches 2; Indel8 GCTGGGCAGGGTGGCACAGT 975 N l Similarity 90.0 18; Conservative 926 Query Match Local Best Loca Matches

21 GCTGGGCAGGATGGCAAGT 원

RESULT 558 AAA64547/c

AAA64547 standard; DNA; 23 BP

AAA64547;

(first entry) 02-JAN-2001

Nucleotide sequence of a donor site of human FEZ1 gene.

Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth; tumour proliferation; tubulin; microtubule; protein EF1-gamma; tubulin polymerisation disorder; mitosis initiation; cell proliferation; cell growth; cell shape; cell rigidity; cell motility; DNA replication; tumorigenesis; tumour survival; metastasis; ss.

Homo sapiens.

WO200050565-A2

31-AUG-2000

25-FEB-2000; 2000WO-US04950

25-FEB-1999;

99US-0121537

(UYJE-) UNIV JEFFERSON THOMAS

Ishii H; Croce CM, WPI; 2000-558396/51

New polynucleotide homologous with a portion of one strand of the human FEZ1 gene, useful for alleviating abnormal cell proliferation such as cancer

Example 1; Page 103; 255pp; English.

AAA64539-50 represent donor and acceptor sites of the human FEZ1 gene. FEZ1 is a tumour suppressor gene, located at chromosome location 8p22. Decreased or no expression of FEZ1 is detected in a variety of cancer cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts with tubulin, with microtubules,

and with protein EFI-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FEZI protein.
Inhibitors of FEZI gene expression are useful for inducing cells to proliferate. Compounds which modulate FEZI association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility rate and stage of cellular DNA replication; intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FEZI binding and phosphorylation are also useful for and metastatic such as tumorigenesis, tumour survival, growth and metastasis. 8X333333333333333X8

Sequence 23 BP; 6 A; 4 C; 10 G; 3 T; 0 other;

0 1.5%; Score 16.8; DB 1; Length 23; 90.0%; Pred. No. 2.7e+02; Indels Mismatches , Conservative Query Match Best Local Similarity Matches 18; Conserv

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Gaps

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RESULT 559 AAV06320, AAV06320 standard; DNA; 24 BP

AAV06320;

(first entry) 06-MAY-1998

Human prolyl 4-hydroxylase alpha subunit amplifying 3' primer.

Collagen; human; recombinant; post-translational enzyme; procollagen; prolyl 4-hydroxylase alpha subunit; PCR primer; ss.

Homo sapiens Synthetic.

WO9738710-A1.

23-OCT-1997.

97WO-US07300 11-APR-1997;

96US-0631336 (FIFI-) ACAD FINLAND 12-APR-1996;

Kivirikki KI, Pihlajaniemi T;

FIBROGEN INC

FIBR-)

WPI; 1997-526203/48

Recombinant production of (pro)collagen having correct folding using vectors encoding collagen sub:unit and collagen post-translational enzyme respectively

Example 10; Page 57; 90pp; English

This primer is used to mutate a plasmid pBS(SK-) by PCR by introducing a NotI site upstream of the initiation codon for human prolyl 4-hydroxylase alpha subunit. This is used in the construction of recombinant vectors containing collagen polypeptide enzymes. A novel method for producing a (pro) collagen polypeptide comprises culturing a host cell, where the host expression vector comprising a polynuclectide molecule having a mucleic acid sequence which encodes a (pro) collagen subunit and a second expression vector comprising a polynuclectide molecule having a nucleic acid sequence which encodes a (pro) collagen molecule having a nucleic acid sequence which encodes at least one (pro) collagen post-translational

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enzyme or enzyme subunit. The (pro)collagen polypeptide is then purified from the cultured cell. The (pro)collagen polypeptide is selected from collagen types IV, V. IV. VII., IX, X. XI, XII, XII, XIV, XV, XV, XVI, XVII, XVIII, and XIX. The methods can be used for the production of collagens such as human collagens which can be used in therapeutic applications. The method provides for the synthesis of correctly folded proteins so that they exhibit the normal triple-helical conformation characteristic of procollagens and collagens. Purification of the collagens is greatly facilitated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; translation initiation factor subunit e1F4E binding protein 17.27; publy development malformation; tumour; diabetes; menoxenia; peptic ulcer; translation initiation factor; e1F4E; binding protein; PCR; primer; 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human translation initiation factor eIF4E binding protein 17.27 primer#2.
                                                                                                                                                                                                                                                                                                                                                                       1.5%; Score 16.8; DB 1; Length 24; 90.0%; Pred. No. 2.8e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 7 A; 6 C; 4 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN85224 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000CN-0119722
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                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1339492-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN85224;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 560
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0;

Gaps

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New polypeptide-human translation initiation factor subunit eIF4E binding protein 17.27 for treating embryo development malformation, tumors, diabetes, menoxenia, and peptic ulcer

Example 3; Page 20 (Disclosure); 33pp; Chinese.

The present invention relates to human translation initiation factor subunit eIP4E binding protein 17.27 (see ABB83427). The protein and its coding sequence are useful for treating various diseases, such as embryo development malformation, tumours, diabetes, menoxenia, peptic ulcer, etc. The present sequence is a PCR primer, which was used in an example from the invention

Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;

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Gaps
                                                                             ;
0
Query Match
1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2.88+02;
Matches 18; Conservative 0; Mismatches 2; Indels
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1081 ATTAAAAAAAAAAAA 1100

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Human tumour necrosis factor receptor mRNA, AIDS; modified, HIV;
RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                        Oligomer TNFR941 for forming triplex with HUMNFR target duplex.
                                                                                                                                                                                   /*tag= b
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                       New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
                                                                                                                                                                                                                                                                                                                                            Milligan J;
                                                                                                                                                                                                                                                                                                                                          Matteucci MD,
                                                                                                                                               Location/Qualifiers
21 ATTCAAAAAAAAAAAACA
                                       BP
                                                                                                                                                                                                                                                              90US-0643382.
91US-0683420.
91US-0686544.
91US-0686546.
91US-0686547.
                                                                                                                                                             /*tag= a
/mod_base=
                                                                                                                                                                                                                                                91WO-US08811
                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                          Krawczyk S,
                                     AAQ30446 standard; DNA;
                                                                                                                                                                                                                                                                                                                          (GILE-) GILEAD SCI INC.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-217083/26.
                                                                                                                                              Key
modified_base
                                                                                                                                                                          modified_base
                                                                                                                                                                                                                WO9209705-A1
                                                                                                                                                                                                                                               25-NOV-1991;
                                                                  25-MAR-2003
07-DEC-1992
                                                                                                                                                                                                                                                                      18-JAN-1991;
08-APR-1991;
                                                                                                                                                                                                                                                                                                            27-SEP-1991;
                                                                                                                                                                                                                                 11-JUN-1992
                                                                                                                                                                                                                                                                                                    17-APR-1991
                                                                                                                                                                                                                                                                                                                                          Froehler B,
                                                                                                                                                                                                                                                                                     17-APR-1991
                                                                                                                                                                                                                                                                                            17-APR-1991
                                                                                                                               Synthetic.
                                                    AAQ30446;
                     RESULT 561
AAQ30446/c
                                     셤
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See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PD field.) BP; 1 A; 1 C; 0 G; 16 T; 0 other; Sequence 18

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harsh conditions.

The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumnour necrosis factor receptor mRNA beginning at nucleotide 234 contg. a purine rich sequence concd. on strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA tumnours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to

Claim 12; Page 72; 77pp; English.

Length 18; 1.5%; Score 16.4; DB 1; 94.4%; Pred. No. 2.4e+02; Query Match Best Local Similarity

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12-JUL-2001
                                                                                                                         10-MAY-2001
                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF99943;
                                                                                                                                                                                                                                 Oste CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 564
AAF99943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                     Key
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
0
                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptors where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes.
                                                                                                                                                                                                                                                                                                                            Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                 Binary encoded sequence tag; BEST; nucleic acid analysis; gene expression; adaptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
Indels
                                                                                                                                                                                                                                                                                            Latimer DR;
                                                                                                                                 Binary encoded sequence tag method anchored primer #3.
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.4; DB 1;
Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-aminopurine substituted region of an RP-TFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                           Feng L,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 101; 101pp; English.
                                                                                                                                                                                                                                                                                           PM,
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                1100
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                                                                                                                                                                                                                                                                                           Lizardi
                                                                             AAF75598 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS05715 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.48;
                1083 TAAAAAAAAAAAAAA
                                  18 таааааааааааааа
                                                                                                                                                                                                                              11-AUG-2000; 2000WO-US22164.
                                                                                                                                                                                                                                               13-AUG-1999; 99US-0148870.
06-APR-2000; 2000US-0544713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082 TTAAAAAAAAAAAAA
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                                                                                                               (first entry)
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17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                           Roth ME,
                                                                                                                                                                                                                                                                                                                                                        and adaptor-indexers
                                                                                                                                                                                                                                                                                                           WPI; 2001-202878/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                         (UYYA ) UNIV YALE
                                                                                                                                                                                            WO200112855-A2.
                                                                                                                                                                                                                                                                                           JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                               10-MAY-2001
                                                                                                                                                                                                             22-FEB-2001
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                              AAF75598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS05715
                                                                                                                                                                                                                                                                                           Kaufman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 563
Matches
                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is a second reverse phase triplex forming oligonucleotide, RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (DNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonuclectide and probe to target sequence -
reverse phase triplex forming oligonucleotide, RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysing target nucleic acid sequences, useful for population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                               "Other= Hypoxanthine or Inosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide purification; liquid chromatography;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 1;
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 1 other;
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 66; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1099
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                                                                                                                                                                                                                                                    /*tag= a
/label= "OTHER"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic oligonucleotide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AANAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1999; 99US-01633416.
03-NOV-1999; 99US-0163416.
21-DEC-1999; 99US-0171348.
07-JUL-2000; 2000US-0216579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-2000; 2000WO-US30534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humans, plants and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF99943 standard; DNA;
                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramberg ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-343488/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CYGE-) CYGENE INC. (OSTE/) OSTE C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          WO200132929-A1
                                                                                                                                                                                                                modified base
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The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:II is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention.
                                                                                                                                                              Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen; probe; cellular adhesion modulator; cellular proliferation modulator; human retrovirus; non-human retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel composition comprising a number of sensor arrays, where each array comprises a unique probe oligonuclectide, which is the reverse complement of part of a unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions comprising sensor arrays made up of unique probe oligonucleotides - useful for characterizing a sample of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%; Score 16.4; DB 1; 34.4%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deletion sequence oligonucleotide 30.
                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 9; Page 99; 163pp; English.
                                                                                                                                                                                                                                              Example 1; Page 6; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1082 TTAAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.48;
      03-MAY-2000; 2000EP-0109436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TTCAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US18084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0923771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX23577 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.49
Watches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deletion oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                    Schroeder KH, Koike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Srivatsa GS;
                                                                                                                          WPI; 2002-068256/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-205198/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9911820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX23577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX23577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as polystyrene resin;

(b) pouring a mixed developing solvent composed of a buffer made from a volatile salt and a water soluble organic solvent at a suitable concentration gradient into the column;

(c) pouring an acid, particularly 6-16 v/v* acetic acid, into the column to deprotect the oligonucleotides protected with the hydrophopic group;

(d) pouring a mixed developing solvent composed of a buffer made from a hydrogencarbonate solution adjusted at pl# 8-10, and a water soluble organic solvent at a suitable concentration gradient to elute the deprotected oligonucleotides; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an oligonuclectide provided in a specification relating to the simplified purification of oligonuclectides by liquid chromatography. The process comprises:

(a) pouring oligonuclectides protected with a hydrophobic group and oligonuclectide with no protective group into a liquid chromatography column packed with an acid and alkali resistant packing agent, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                         process for purification of oligonucleotides using liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 16.4; DB 1; Length 20; 94.4%; Pred. No. 2.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     removal of the solvent and the salt from the eluted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
  ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 other;
  protective group; deprotection;
                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 4; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1100
                                                                                                                                                                                                                                         (TOAG ) TOA GOSEI CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                 99JP-0154974.
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                                                                                                                                                              99JP-0154974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TAAAAAAAAAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA05916 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                             WPI; 2001-268251/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotides.
                                                                           JP2000342265-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                        chromatography
                                                                                                                                                           02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1152063-A1.
                                                                                                                                                                                                 02-JUN-1999;
hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-2002
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                                     Synthetic.
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ABA05916;

RESULT 565 ABA05916/

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Gaps

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target oligonucleotide present in a mixture of target deletion sequence oligonucleotides. The compositions form a method for characterizing a sample of target deletion oligonucleotides which are labelled and hybridize with the probe oligonucleotides of the sensor arrays. Such oligonucleotides and their targets are represented in AAX23548-X23709 oligonucleotides and their targets are represented in AAX23548-X23709 oligonucleotides characterized by the method form pharmaceutical compositions that are useful for modulating cellular adhesion or proliferation, and being active against a eukaryotic pathogen, a human retrovirus, including influenza virus, Epstein-Barr virus, Respiratory Syncytial Virus or cytomegalovirus (CMV). The compositions enable characterization of deletion sequence oligonucleotides having related, but different nucleobase sequences, and quantification of different species of deletion sequence ("target") oligonucleotides in a mixture. Also, if the specificity of the oligonucleotide's nucleobase sequence con in the reverse complement is not modified, the method may be performed
                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel method of stabilizing duplex formation, or destabilizing non-specific duplex formation using primer containing modified nucleotide analogs, useful for preventing mispriming during PCR, RACE,
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; destabilise non-specific duplex formation; PCR; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purification; sequencing; genetic marker; RACE; DNA synthesis; ss
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                 Length 23;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                          Query Match
1.5%; Score 16.4; DB 1;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/mod_base= i
/note= "inosine"
                                                                                                                                                                                                                                                                                                                                                                                                             1082 TTAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/mod_base= i
/note= "inosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TTCAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic oligonucleotide #1
                                                                                                                                                                                                                                                                              using oligodeoxynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA synthesis or sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-CA00933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA29753 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Das M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-328943/28.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA29753;
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AAA29753/c
       DDDDDDDDDDDDDDDDDDDX8
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                                                duplex formation, between an oligonucleotide and a target nucleic acid (NA), comprising incubating the target NA with a modified oligonucleotide (T) comprising a homopolymeric sequence having a modification which decreases or abrogates H-bonding between the modified oligonucleotide and the non-specific target NA. The modified homopolymeric sequence and a non-homopolymeric target sequence. It is used to increase the proportion of full length cDNA clones for a library, to reduce mispriming during sequencing, 5' or 3' RACE (rapid amplification of cDNA ends) or DNA synthesis or to generate bona fide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for producing a human antibody phage display library (1), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display
                                     invention describes a method for destabilising non-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antibody; immunoglobulin; interleukin 8; ILB; immunogen; human antibody phage display library; immunisation; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a human antibody phage display library comprises providing
                                                                                                                                                                                                                                   genetic markers. The present sequence represents an oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                   ,
                                                                                                                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                            1.5%; Score 16.4; DB 1; Length 2
85.0%; Pred. No. 3.1e+02;
Artive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human interleukin 8 antigen sequencing primer C.
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(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                                                                                                                                                                                                                                                          Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 23; Page 102; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  1081 ATTAAAAAAAAAAAAA 1100
Example 1; Page 25; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gray J,
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99US-0453234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH30031 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-335567/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1999;
01-DEC-1999;
                                       present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH30031;
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 568
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Example 24; Page 103; 161pp; English Gray J, 997 GTCTGAGGCTGGAGAATG 1014 AAH30035 standard; DNA; 23 BP. 94.48; 18 Grcrcacctrcacatic 99US-0157415. 99US-0453234. 02-OCT-2000; 2000WO-US27237. (first entry) Conservative Buechler J, Valkirs G, WPI; 2001-335567/35. Best Local Similarity Matches 17; Conserv WO200125492-A1. PCR primer; ss 02-OCT-1999; 01-DEC-1999; 19-JUL-2001 12-APR-2001 Synthetic. AAH30035; Query Match RESULT 569 Homo AAH30035 888888888888 ઠે 셤

Ö library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human moncolonal antibodies humans with antigens, and the difficulties faced with immortalising B humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAR29958 to AAR30666 and AAR34994 to AAR35056 represent sequences used in the exemplification of the present invention. The present invention describes a method (M1) for producing a human antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprises a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be the method acids encoding antibody chains obtained from Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immorralising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056 Human, antibody, immunoglobulin, interleukin 8, ILB, immunogen, human antibody phage display library, immunisation, transgenic animal, Gaps Human myelin proteolipid protein (PLP) antigen sequencing primer C. · 0 1.5%; Score 16.4; DB 1; Length 23; 94.4%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels (BIOS-) BIOSITE DIAGNOSTICS INC. (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC. Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other; Lonberg N;

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(X) m5 - (alpha)n-beta-N3'; or (X) m5' - (gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or Ni; V = adenine, gamma = thymine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; gamma = thymine; which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.
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represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - useful as primers
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                                                              23;
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                                                                                          1; Indels
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ve 1; Mismatches 0; Indels
                                                                Length
                                                           Score 16.4; DB 1;
Pred. No. 3.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides having at least two new nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;
                                Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                     RT-PCR primer of the invention SEQ ID 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 12; 19pp; Japanese.
                                                                                                                 997 GTCTGAGGCTGGAGATG 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 TAAAAAAAAAAAAA 1099
                                                                                                                                            18 Grendaggerraagaarg 1
                                                                                                                                                                                                                      BP.
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                                                          1.5%;
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                                                                                                                                                                                                    AAX18389/c
ID AAX18389 standard; DNA; 18
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                                                                                                                                                                                                                                                                          (first entry)
                                                 Query Match
Best Local Similarity 94.4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        JP11032765-A
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                                                                                                                                                                                                                                                                          11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                               AAX18389;
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                                                                                                                                                                                       RESULT 570
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Polymorphic sequence for ABC1 polymorphic site #38
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                                                                                                                                                                                                                                                                                             (UYBR-) UNIV BRITISH COLUMI
(XENO-) XENON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-244356/25.
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es 18: Conserv
                                                                                                          WO200115676-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                             08-MAR-2001
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, previous and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ5812-Z26825 represent human polymorphic sites described in the method of the
                                                                             Polymorphism, human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plague, dysplastic lesions, endometriosis or graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 16.2; DB 1;
85.7%; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanton VP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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                                                  Human polymorphic region 752.
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             (first entry)
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    (VARI-) VARIAGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Housman D, Ledley FD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-521232/44
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                      WO9841648-A2
                                                                                                                                                                                                                                                                                                                              19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1997;
             30-NOV-1999
                                                                                                                                                                                                                                                                                           24-SEP-1998.
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AAF93028
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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a lower than normal high density lipoprotein-cholesterol (HDL-0) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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.larity 81.8%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pimstone SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    991 TTGGAAGTCTGAGGCTGGAGAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 317pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958.
                                                                                                                                                                                                                                                                            01-SEP-2000; 2000WO-IB01492.
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Gaps

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Length 16;

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WPI; 1999-095671/08.
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                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                        DNA chip primer #4.
                                                                                                                                                           WO200061594-A2
        Agostino MJ,
                                                                                             16;
                                                                                                                                   22-FEB-2001
            Merberg D,
                                                                                                                                                                 19-0CT-2000
                                                                                                                                                      Synthetic.
                                                                                                                             AAC66068;
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                                                                                                                  RESULT 574
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This invention describes nucleoside derivatives (I) with photolabile protecting groups. (I) are used to synthesize oligonucleotides using the photolithographic nucleic acid chip method, particularly where these are intended for performing enzymatic reactions initiated from a free reactions, but also reverse transcription, cDNA synthesis etc.), also for hybridization testing, sequenoing and in DNA computing. (I) are produced with high selectivity by reaction with a mild acylating agent that has high specificity for the 3'-position, without significant side-reactions (cf. more reactive acylating agents such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Branched compounds useful in e.g. nucleic acid synthesis reaction comprises nucleic acid moieties optionally extended by a polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branched chain compound; nucleic acid synthesis; primer extension; reverse transcription; nucleic acid hybridization; nucleic acid amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonuclectide used to produce branched chain compounds.
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                Score 16; DB 1; L
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                          Sequence 16 BP; 16 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                    Mismatches
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"branch present"
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"COOH attached"
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"COOH attached"
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                                                                                                                                                                                                                                                                                        1.5%;
100.0%; Pre
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              Disclosure; Fig 9; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH42481 standard; DNA; 16 BP
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Best Local Similarity 100.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH42481,
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                                                                                                                                                                                                                    The sequence is that of the 3' end of a sequence encoding a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no autivity, cytokine and cell proliferation/differentiation activity, immune stimulating (a. as vaccines) or suppressing activity, activity, activity, chemotactic/chemokineic activity, activity, chemotactic/chemokineic activity, activity, chemotactic/chemokineic activity, add thrombolytic activity, receptor/ligand activity, anti-inflammatory and thrombolytic activity, receptor/ligand activity, anti-inflammatory inhibition activity, respectiviliqued activity, anti-inflammatory inhibition activity. It is also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA chip; primer; nucleoside derivative; photolabile protecting group; photolithographic nucleic acid chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleoside derivatives with photolabile protecting groups, useful in oligonucleotide synthesis, particularly on solid phases, e.g. for hybridization testing -
                                                                                                                       New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                           Mccoy JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
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                                       Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 16; DB 1; Le
100.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ....
                                                                                                                                                                                        Disclosure, Page 54; 76pp; English.
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                                      Jacobs K,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084 AAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1999; 99DE-1015867.
28-JAN-2000; 2000DE-1003631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC66068 standard; DNA; 16
 (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                       Evans C,
                                                      Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoheisel J;
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fluorescence. Upon hybridisation to the complementary target sequence there was an increase in fluorescence yield, measured as the ratio of the fluorescence emitted by the hybrid between the ODN-MGB-LF conjugate and its target sequence to the fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.

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Gaps

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Length 16; Indels

Score 16; DB 1; Lenc ;; Pred. No. 2.5e+02;

1.5%; Scur 100.0%; Pre 0; '

1084 AAAAAAAAAAAA 1099

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16; Conservative

Matches

Local Similarity

Query Match

16 ААААААААААААА

AAF30895/c ID AAF30895 standard; DNA; 16

Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

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acid moieties optionally extended by a polymerase. The branched chain compounds of the invention are used in nucleic acid synthesis reaction, primer extension reaction, reverse transcription reaction of RNA into DNA, nucleic acid hybridization experiment (for identifying sequence a nucleic acid), and nucleic acid amplification experiment (for analysing the expression pattern of genes). The compounds are also used in solid-phase enzymatic reactions. The present sequence was used in the course of the invention to produce branched chain compounds.
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe;
    compounds containing nucleic
                                                                                                                                                              ;
0
                                                                                                                                    1.5%; Score 16; DB 1; Length 16; 100.0%; Pred. No. 2.5e+02;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                           Oligonucleotide portion of ODN-MGB-LF conjugate.
                                                                                                             Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
                                                                                                                                         100.08; Pred. ...
specification describes branched
                                                                                                                                                                               1084 AAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                           AAF30880 standard; DNA; 16
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                    16 AAAAAAAAAAAAA
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3-LF; oligonucleotide; minor groove binder; fluorophore; hybridisation; detection; fluorescence; probe;

Oligonuclectide-minor groove binder complex.

ODN-MGB-LF;

latent

Synthetic.

(first entry)

09-JUL-2001

AAF30895;

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The present sequence is that of an oligonucleotide (ODN)-minor groove binder (MGF) complex. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids. ONN-MGB-LF conjugates of the invention also comprises a latent fluorophore (LF), which binds similarly to the MGB but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or diagnosis, especially (real-time) PCR, for single-nucleotide mismatch discrimination, target or signal amplification, array-based assays and sequencing, including
                                                                                                                                                                                                                                     a
"thymine modified by a minor groove binder
(2-dimethylaminonaphthalene-6-
sulfonamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. single-nucleotide mismatch discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vermeulen NMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 101; 105pp; English.
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           (EPOC-) EPOCH BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2000; 2000WO-US29786.
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modified_base
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for

Conjugate of oligonuclectide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g.

Afonina IA, Vermeulen NMJ;

WPI; 2001-328656/34

Dempcy RO,

(BPOC-) EPOCH BIOSCIENCES INC

99US-0428236

26-OCT-1999;

single-nucleotide mismatch discrimination

Disclosure; Page 58; 105pp; English.

The present sequence is that of the oligonucleotide (ODN) component of an ODN-MGB (minor groove binder)-LF (latent filuorophore)
Conjugate of the invention. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or diagnosis, especially (real-time) PCR, for single-nucleotide array-based assays and sequencing, including detection, of double-stranded DNA by triplex formation. Many different targets can be detected a single reaction vessel. The present ODN-MGB-LF

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(first entry)

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Oligonucleotides analogues useful in detection, separation and purification of nucleic acid molecules, comprise monomers, dimers and
                                                                                                                                                             Nucleotide sequence of oligomer \# 1 used to test thermal stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;
                                                                                                                                                                                              Protein nucleic acid molecule; PNA; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page 118; 197pp; English.
                                                                   ABA97402 standard, DNA; 16 BP
                                                                                                                                                                                                                                                                                                                        13-MAR-2001; 2001WO-US08111.
                                                                                                                                                                                                                                                                                                                                                      14-MAR-2000; 2000US-189190P.
                                                                                                                                                                                                                                                                                                                                                                                                     (ACTI-) ACTIVE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-041177/05.
                                                                                                                                                                                                                                                           WO200168673-A1.
                                                                                                                                18-JUN-2002
                                                                                                                                                                                                                                                                                          20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   Efimov V.
                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligomers
                                                                                                  ABA97402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                    ABA97402
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                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an analytical support, to which a number of oligonucleotides are fixed. The oligonucleotides are labelled with a fluorescent compound, the fluorescence of which varies when the oligonucleotide hybridises to its complement. The analytical support is useful in hybridisation testing for identification of specific nucleic acids, such as genomic sequencing, detecting mutations or pharmaceutical development. The present oligonucleotide was used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "OTHER = F1(CH2)6-PO-thymine, where F1 is flavine
and PO is a phosphate group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               where
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Support for hybridization analysis of nucleic acids for sequencing techniques, comprises an array of oligonucleotides having a label the fluorescence changes follow hybridization
                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                              Analytical support; genomic sequencing; mutation detection; pharmaceutical development; ss.
                                                            1.5%; Score 16; DB 1; Length 16;
100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ິບ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dueymes
detection of double-stranded DNA by triplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fontecave M, Decout JL,
                             Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 12; 33pp; French.
                                                                                                                           1084 AAAAAAAAAAA 1099
                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-2000; 2000FR-0002236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2000; 2000FR-0002236
                                                                                                                                                                                                                                      ABA04585 standard; DNA; 16
                                                                                                                                                (first entry)
                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peltie P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-628265/73.
                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                Oligonucleotide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2805348-A1
                                                                                                                                                                                                                                                                                                 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuzin M,
                                                                                                                                                                                                                                                                   ABA04585
                                                              Query Match
                                                                              Best Loca
Matches
                                                                                                                                                                                                     RESULT 578
                                                                                                                                                                                                                     ABA04585/
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This invention relates to oligonucleotide analogues comprising a protein nucleic acid molecule (PNA) monomer. They are used in the detection and separation of nucleic acid molecules and as probes, primers, linkers, adapters and antisense agents on solid supports. Modifications enhance their use as capture and detection probes e.g. by the incorporation of biotin, digoxigenen, radioiscopes, fluorescent labels such as Iluorescein and reporter molecules such as alkaline phosphatase. They are also used for enhancing or inhibiting the activity of an enzyme proteases, have high affinity, binding specificity and solubility. The polyamide backbone of PNAs is resistant to both nucleases and proteases. PNAs bind nucleic acid molecules with greater affinity than DNA or RNA concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence the thermal represents a DNA oligomer which is used to represent the thermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 16; DB 1; Le
100.0%; Pred. No. 2.5e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084 AAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL54078 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL54078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 580
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ID AALS.
XX
AC AALS.
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Gaps

0

0; Indels

1.5%; Score 16; DB 1; Length 16; 100.0%; Pred. No. 2.5e+02;

100.0%; Pred. No.

Conservative

Local Similarity les 16; Conserv

Matches

Query Match

1084 AAAAAAAAAAAA 1099

AAAAAAAAAAAAA

91

a 8

(first entry)

28-JUL-1999

AAX69800;

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Detection; single-stranded sensor; detectable fluorescence emission; forensic testing; paternity testing; tissue typing; hereditary disorder; human population genetics; human evolutionary history; cystic fibrosis; human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
                                                                                                                                                                                                                                      Detecting polynucleotides, for pharmacogenetic testing, comprises contacting a target polynucleotide with a complementary single-stranded sensor polynucleotide and an agent that allows the sensor to fluoresce
         Oligo-homodeoxyribonucleotide sequence, oligo dT,
                                                                                                                                                                                                                                                                                      Example 1; Page 25; 41pp; English.
                                                                                                                                                                                                    Stucky GD
                                                                                                                                   16-APR-2002; 2002WO-US12176.
                                                                                                                                                      L6-APR-2001; 2001US-0836579
                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
(CHAJ/) CHA J N.
                                                                                                                                                                                                  Cha JN, Morse DE,
                                                                                                                                                                                                                     WPI; 2003-103378/09
                                                                                                                                                                                                                                                                      upon excitation
                                                                                             WO200284271-A2
                                                                          Unidentified.
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The invention relates to a novel assay for detecting a polymucleotide in a sample, which comprises: contacting a sample suspected of containing a carget polymucleotide with a predetermined single-stranded sensor carget polymucleotide complementary to the target polymucleotide, in a solution comprising an agent that is a nonaqueous solvent that allows the sensor polymucleotide; and detertable fluorescence emission, exciting the sensor polymucleotide; and determining fluorescence emission. The assay is useful for detecting a single or double-stranded target colymucleotide, such as, DNA or RNA in a sample. The assay finds use in a view variety of different applications including pharmacogenetic testing, wide variety of different applications including pharmacogenetic testing, control of dentify the species or individual which was the forensic specimen, in anthropological setting, paternity compatibility between prospective tissue or blood concre and patients and in screening for hereditary disorders. The method concre and patients and in screening for hereditary disorders. The method is also useful to study alterations of gene expression in response to a stimulus, disease, drug or medication, and other applications include characterisation of human haplotype diversity. The method is useful for detecting polymucleotide sequences from contaminants or pathogens contautions polymorphisms, which may be associated with particular alleles or subsets or alleles. The method is useful for detection of mutations and to detect culcular applications expenses to disorders including cystic fibrosis. Tay-Sachs, and sickle-cell anaemia. This polymucleotide sequence represents an oilgonucleotide sequence represents an ail sickle-cell anaemia. This polymucleotide sequence represents an oilgonucleotide sequence represents an and sickle-cell anaemia.

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Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
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Length 16; 0; Indels Score 16; DB 1; Le Pred. No. 2.5e+02; 1.5%; ... 100.0%; Pred. No. -Local Similarity 100. Query Match Matches

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Gaps

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AAX69800 standard; RNA, 17 BP. RESULT 581 AAX69800/

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The present invention describes mucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (IL-1), kinase insert domain containing angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                          Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                           Human flt1 VEGF receptor hammerhead ribozyme substrate #1095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 1; Le
Pred. No. 2.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             McSwiggen J, Pavco P, Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 0 A; 1 C; 0 G; 16 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Sc.__
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 79; 218pp; English.
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                                                                                                                                                                                                                                                                                                                                                 95US-0005974.
                                                                                                                                                                                                                                                                                                     96WO-US17480.
                                                                                                                                                                                                                                                                                                                                  96US-0584040.
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                                                                                                                                                                                                                                                                                                                                                                                             (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX69801 standard; RNA; 17
                                                                                                                                                                          liver kinase 1; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-259017/23.
                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                     WO9715662-A2
                                                                                                                                                                                                                                                                                                   25-OCT-1996;
                                                                                                                                                                                                                                                                                                                               11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                              26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             Escobedo J,
                                                                                                                                                                                                                                                                      01-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX69801;
                                                                                                                                                                          foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 582
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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X) ms^5 - (alpha)n-beta-Ns', or (X)ms^5 - (gamma)k-delta-Ns', where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

M = 0 or 1; alpha = thymine; n = adenine, gamma = trymine;

N = adenine, gaunine or cytosine or thymine;

k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine,
                                                                                                                                                                                                                                                     AAV49503-V49507 are primers used in the isolation of a human eosinophil cell activator. This protein and antibodies gamerated from the protein can be used for treatment and diagnosis of malignant tumours, parasitic inflections, allergic inflammation, eosinophilic pneumonia, rapid onset eosinophila, and autoimmune diseases. DNA can be used for diagnosis, and the antisense DNA in gene therapy of these disorders. The protein can be used for screening of potential agonists or antagonists of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - useful as primers in
                                                                                                                                                activates eosinophil cells - for infection, autoimmune disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 1; Leng
;; Pred. No. 2.7e+02;
                                                       Saito A;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides having at least two new nucleotides
                                                     Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT-PCR primer of the invention SEQ ID 12.
                                                                                                                                                                                                                   Example 1; Page 64; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 11; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Scc...
100.0%; Pre
                                                   Nakagawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083 TAAAAAAAAAAAA 1098
                                                                                                                                          DNA and encoded protein which treatment of cancer, parasite
         (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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AAX18371 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 TAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                             Kuga T, Naka
, Yoshisue H;
                                                                                                                                                                                allergic inflammation
                                                                                                        WPI; 1998-333261/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11032765-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16,
                                                                   Shinkai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX18371;
                                                 Koike M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT-PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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           à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fins-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
88
                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bosinophil cell activator; treatment; diagnosis; malignant tumour; parasitic infection; allergic inflammation; eosinophilic pneumonia; rapid onset eosinophilia; autoimmune disease; gene therapy; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                        McSwiggen J, Pavco P, Stinchcomb D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human eosinophil cell activator HVC002 primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 1 C; 0 G; 16 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV49503 standard; cDNA to mRNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 79; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 AAAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                      96WO-US17480
                                                                                                                                                                                       96US-0584040.
                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
foetal liver kinase 1;
                                                                                                                                                                                                                                                                                                                                          WPI; 1997-259017/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                       Homo sapiens
                                                                           WO9715662-A2
                                                                                                                                                  25-OCT-1996;
                                                                                                                                                                                                           26-OCT-1995;
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                                                                                                                01-MAY-1997.
                                                                                                                                                                                                                                                                                                        Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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Query Match

Matches

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Gaps

0;

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guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.
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8888**8**

Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 other;

Query Match
1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 1083 TAAAAAAAAAAAA 1098

ô

Gaps

ö

16 TAAAAAAAAAAAA 1

AAC64161 standard; DNA; 17

AAC64161;

BP.

PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.

(first entry)

21-FEB-2001

Human, pollinosis-associated gene 581, IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065048-A1

02-NOV-2000

26-APR-2000; 2000WO-JP02732.

99JP-0120492 27-APR-1999;

(GENO-) GENOX RES INC.

Gunji Obayashi M, Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K; Sugita Y, , Imai Y, Obayashi I, Nagasu T,

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Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 38; 46pp; Japanese.

WPI; 2000-687341/67.

Pollenosis-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates

Example 6; Page 39; 69pp; Japanese.

The invention relates to the human pollinosis-associated gene 581 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates pollen using to the protein encoded by pollinosis-associated gene 581; to expression constructs and host cells comprising pollinosis-associated gene 581; to expression nucleic acids; pollinosis-associated gene 581 primers and probes; or antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 581 nucleic acids; and a method of cid pollinosis-associated gene 581 nucleic acids. The invention additionally encompasses methods of screening the expression of pollinosis-associated gene 581 nucleic acids. The invention additionally encompasses methods of screening the expression of pollinosis-associated gene 581 in pollen control. Pollinosis-associated gene 581 in pollen control. Pollinosis-associated gene 581 in the lagnosis of a control. Pollinosis-associated gene 581 is useful in the diagnosis of a lergic diseases and in the screening of drug candidates for the reatment of such diseases. The present sequence represents a PCR primer custom the isolation of human pollinosis-associated gene 581 cDNA.

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

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0
                                                                                                                                                                                                                                                                                                   Gunji S;
                   Gaps
                                                                                                                                          PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
                   0
                                                                                                                                                          Human, pollinosis-associated gene 513, IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                   Obayashi M,
1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 2.7e+02;
tve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Sugita Y, Kashiwabara T, Oshida T, Obay
, Imai Y, Yoshida N, Ogawa K, Matsui K;
1.55,
100.0%; Pre
                                 1083 TAAAAAAAAAAA 1098
                                                                                          AAC64171 standard; DNA; 17 BP
                                                                                                                                                                                                                                              26-APR-2000; 2000WO-JP02733.
                                                                                                                                                                                                                                                                99JP-0120491.
                                                                                                                           (first entry)
                                                 17 TAAAAAAAAAAAAA
       Local Similarity 100.
                                                                                                                                                                                                                                                                               (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                                                          WPI; 2000-687342/67.
                                                                                                                                                                                                             WO200065049-A1.
                                                                                                                                                                                                                                                               27-APR-1999;
                                                                                                                          21-FEB-2001
                                                                                                                                                                                                                               02-NOV-2000.
                                                                                                                                                                                                                                                                                                        Obayashi I,
                                                                                                                                                                                             Synthetic
                                                                                                           AAC64171;
                                                                                                                                                                                                                                                                                                 Nagasu I,
Query Match
      Best Loca
Matches
                                                                         RESULT 586
                                                                                  AAC64171
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The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen cusing the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 513 nucleic acids; and method of dagnosis of allergic diseases via the detection of pollinosis-associated gene 513 nucleic acids; and methods of screening drug candidates for the treatment of allergic disease by measuring the cypression of pollinosis-associated gene 513 in pollen antigen-stimulated companies of a test compound relative to a control.

Pollinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer cused in the isolation of human pollinosis-associated gene 513 cDNA. Length 17; / Match
Local Similarity 100.0%; Pred. No. 2.7e+02;
les 16; Conservative 0; Mismatches 0; Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other; Query Match

1083 TAAAAAAAAAAAA 1098

Matches

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.; 0

Gaps

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Indels

TAAAAAAAAAAA 2 17

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The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from the formation of the control of the protein encoded by pollinosis gene control of the invention also relates to the protein encoded by pollinosis gene the invention also relates to the protein encoded by pollinosis gene and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 419 mucleic acids; pollinosis-associated gene; methods of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 nucleic acids. The invention additionally encompasses of disease by measuring the expression of pollinosis-associated gene 419 in collinosis-associated gene 419 in the present of allergic pollinosis-associated gene 419 in the present of allergic collinosis-associated gene 419 in the present sequence represents a proportion of the treatment of such diseases. The present sequence represents
                                                                                                                                            PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pollinosia-associated gene 419 undergoing significantly low exp in subjects with high cedar pollen-specific IgB levels, useful diagnosis of allergic diseases and screening drug candidates -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obayashi M,
                                                                                                                                                                                      Human; pollinosis-associated gene 419; FAF-1 homologue;
Fas-associated factor-1; IgE; immunoglobulin E;
cedar pollen allergy; T-cell; reduced expression; detection;
diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kashiwabara T, Oshida T, Obay
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 49; 77pp; Japanese.
                    AAC64181 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-2000; 2000WO-JP02729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0120490
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687338/67.
                                                                                                                                                                                                                                                                                                                                         WO200065045-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1999;
                                                                                                        21-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obayashi I,
                                                                                                                                                                                                                                                                                                   Synthetic
                                                              AAC64181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagasu T,
AAC64181,
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expression

Gunji S;

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PCR primer used in the isolation of human pollinosis-associated gene. 9 cDNA.
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                         Gaps
                         .;
0
    Length 17;
                        0; Indels
 Score 16; DB 1; Le
Pred. No. 2.7e+02;
                      Mismatches
1.5°,
100.0%; Pre-
                                        1083 TAAAAAAAAAAA 1098
                                                              TAAAAAAAAAAAA 2
                    16; Conservative
          Similarity
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Pollinosie-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                                                 Gunji
                                                               PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
                                                                               Human, pollinosis-associated gene 373; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                              T, Oshida T, Obayashi M,
Ogawa K, Matsui K;
                                                                                                                                                                                                                               Kashiwabara
Yoshida N,
           BP.
                                                                                                                                                                         26-APR-2000; 2000WO-JP02730.
                                                                                                                                                                                          99JP-0120489.
AAC64202/c
ID AAC64202 standard; DNA; 17
                                            (first entry)
                                                                                                                                                                                                           (GENO-) GENOX RES INC.
                                                                                                                                                                                                                             Sugita Y,
I, Imai Y,
                                                                                                                                                                                                                                                         WPI; 2000-687339/67.
                                                                                                                                     WO200065046-A1.
                                                                                                                                                                                          27-APR-1999;
                                            21-FEB-2001
                                                                                                                                                                                                                                       Obayashi I,
                                                                                                                    Synthetic.
                                                                                                                                                                                                                              Nagasu T,
                           AAC64202;
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The invention relates to the human pollinosis-associated gene 373 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-pecific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen cases to the protein encoded by pollinosis gene 373; expression constructs and host cells comprising pollinosis associated gene 373 nucleic acids; pollinosis-associated gene 373 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 373 primers and probes; constructs and sandrated gene 373 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 373 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 373 in pollen context. a control. Pollinosis-associated gene 373 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 373 cDNA.

Example 6; Page 69; 80pp; Japanese.

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0
            Length 17;
                             Indels
Score 16; DB 1; Ler; Pred. No. 2.7e+02;
       Match
Local Similarity 100.0%; Pi
                                              1083 TAAAAAAAAAAAA 1098
                                                                                                               AAC64213 standard; DNA; 17 BP.
                                                                 TAAAAAAAAAAAA
                                                                                                                                 AAC64213;
         Query Match
                           Matches
                                                                                            RESULT 589
AAC64213/c
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                                                                                                               AXA
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Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

0

RESULT 588

17

Query Match

Local

Matches

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Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates
                             PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
                                              Human, pollinosis-associated gene 627; IGE; immunoglobulin B; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                       Kashiwabara T, Oshida
Yoshida N, Ogawa K,
                                                                                                                                                                                                                                                                                              Example 6; Page 41; 51pp; Japanese.
                                                                                                                                               26-APR-2000; 2000WO-JP02735.
                                                                                                                                                                  99JP-0120493
          (first entry)
                                                                                                                                                                                    (GENO-) GENOX RES INC.
                                                                                                                                                                                                       Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                    WPI; 2000-687344/67.
                                                                                                         WO200065051-A1
                                                                                                                                                                  27-APR-1999;
                                                                                                                                                                                                                   Obayashi I,
                                                                                     Synthetic.
                                                                                                                                                                                                        Nagasu T,
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Gunji S;

Oshida T, Obayashi M, wa K, Matsui K;

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The invention relates to the human pollinosis-associated gene 627 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 627 nucleic acids, a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 627 nucleic acids, and a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-cof a test compound relative to a control. Pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
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Gaps
                                 0;
Score 16; DB 1; Length 1,,
Fred. No. 2.7e+02;
Pred. Turnes 0; Indels
           1.5%,
100.0%; Fre
                             16; Conservative
                    Local Similarity
          Query Match
                    Best Loca
Matches
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1083 TAAAAAAAAAAAA 1098
                              17 TAAAAAAAAAAAAA
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AAC64230 standard; DNA; 17 AAC64230; RESULT 59 AAC64230/

21-FEB-2001 (first entry)

PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.

gA nephropathy-associated protein; diagnosis; treatment; antisense;

human; primer; ss.

Homo sapiens. WO9963085-A1

Human IgA nephropathy-associated cDNA primer #61.

(first entry)

10-NOV-2000

Human, pollinosis-associated gene 795, vimentin homologue, IgB; immunoglobulin E; cedar pollen allergy, T-cell; reduced expression, detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

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The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific ISE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis-associated gene 795 constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 795 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids; and a method of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 795 in pollen artigen-siscociated gene 795 in the presence of a test compound relative to antigen-stimulated T-cells in the presence of a test compound relative to antigen-stimulated gene 795 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the creatment of such diseases. The present sequence represents a PCR primer compare the present sequence represents a PCR primer compare the present sequence represents a PCR primer compared gene 795 cDNA.
                                                                                                                                                                                                                                                        Gunji S;
shi E;
                                                                                                                                                                                                                                                                                                                                                               Pollinosis-associated gene 795 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                    Kashiwabara T, Oshida T, Obayashi M, Gun
Yoshida N, Ogawa K, Matsui K, Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 45; Example 6; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083 TAAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                 26-APR-2000; 2000WO-JP02734.
                                                                                                                                                       99JP-0120494
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                                                                                                                                                                                          (GENO-) GENOX RES INC (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                    Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                                                                               WPI; 2000-687343/67.
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                                      WO200065050-A1.
                                                                                                                                                     27-APR-1999;
                                                                                                                                                                                                                                                                    Obayashi I,
                                                                            02-NOV-2000
Synthetic.
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                                                                                                                                                                                                                                                                                             Yokoi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                    Nagasu
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Matches
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IgE

us09904568-1.rng

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Gene highly expressed in patients with high cedar pollen-specific levels, useful for diagnosing pollenosis, and screening candidate
                                                                                    compounds for pollenosis treatment
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98US-0103636.
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Best Local Similarity 100.(
Marches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2000 (first entry)
WPI; 2000-317712/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-013248/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel DNA sequences preferentially expressed in 19A nephropathy patients, and DNA sequences stringently hybridizing to them. Independent claims cover diagnostic reagents for 19A nephropathy incorporating the antisense sequences; the treatment of 19A nephropathy incorporating the antisense sequences for mRNA inhibition; proteins associated with 19A nephropathy, containing sequences encoded by the DNA sequences; antibodies recognizing these proteins; the production of the proteins by culture of host cells transformed with DNA encoding them, diagnostic reagents for 19A nephropathy containing the antibodies, and compositions for the treatment of 19A nephropathy which contain the antibodies. The products of the invention can be used for the diagnosis and treatment of 19A nephropathy. This sequence reperseants a primer used in the isolation and identification of the human 19A nephropathy—associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                  T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
. Takei M, Shibata K, Furuya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pollenosis-associated protein; high pollen-specific immunoglobulin E; IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                     patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer GT15A used in pollenosis associated gene identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
                                                                                                                                                                                                                                                                                         DNA sequences preferentially expressed in 1gA nephropathy proteins encoded by them, and antibodies to those proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 169; 180pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1083 TAAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA30179 standard; DNA; 17 BP
                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK,
                                                    99WO-JP02855
                                                                                             98JP-0152603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98JP-0284610.
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Best Local Similarity
Local 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                  WPI; 2000-097328/08
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                                                28-MAY-1999;
                                                                                             02-JUN-1998;
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           09-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-2000.
                                                                                                                                                                                Ishiwata T,
Sawada S,
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Gunji S;

Obayashi M,

Oshida T,

Kashiwabara T, Lu N, Ogawa K;

Lu N,

Sugita Y, Imai Y,

Nagasu T, S Obayashi I,

(GENO-) GENOX RES INC.

Synthetic

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ଚ 셤 RESULT

AAA30179;

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This sequence represents a PCR primer used in the identification of a human pollanosis associated gene. The gene is highly expressed in individuals with high pollen-specific immunoglobhlin E (IGB) levels. The invention relates to the nucleotide sequence encoding the pollenosis associated protein, diagnosing pollenosis and screening candidate compounds for treating pollenosis. The gene can be used in diagnosing compounds for pollenosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease;
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bellon L;
                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids that interact, and optionally cleave, target
                                                                                                                                                                                                                                                   1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 2.76+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Α̈́,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karpeisky
Haeberli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson JD, Beigelman L, McSwiggen JA, 1
Reynolds M, Zwick M, Jarvis T, Woolf T,
Example 6; Page 38; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 77; Page 79; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences, used to treat cancer
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oestrogen receptor. Because of the high selectivity for targeted Can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA21503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences. AAA22593 to AAA2592 represent their receptor hairpin ribozyme sequences, and AAA26105 represent cestrogen their corresponding target sequences. AAA2293 to AAA25021 represent their corresponding target sequences. AAA2293 to AAA22621 represent their corresponding target sequences and AAA26105 to AAA26212 represent their corresponding target sequences. AAA22621 to AAA22212 represent their corresponding target sequences. AAA22291 to AAA22212 represent cheir corresponding target sequences.
           other conditions associated with levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention.
           for
$55555555555555x8
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Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;

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Gaps
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Score 16; DB 1; Length 1,,
Pred. No. 2.7e+02;
Original Pred. No. 1.00 Pred. No. 2.7e+02;
           1.5%,
100.0%; Pre-
0;
                                16; Conservative
           Query Match
Best Local Similarity
                                  Matches
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AAA25451 standard; DNA; 17 BP RESULT 59.

AAA25451;

(first entry) 19-JUL-2000

Oestrogen receptor hammerhead ribozyme target sequence SBQ ID NO:1949.

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Ношо

WO9954459-A2

28-OCT-1999

99WO-US08547

98US-0082404. 98US-0103636. 20-APR-1998; 23-JUN-1998;

(RIBO-) RIBOZYME PHARM INC

Bellon L; Karpeisky A, Haeberli P; n L, McSwiggen JA, Jarvis T, Woolf T, Beigelman L, Zwick M, Matulic-Adamic J; Thompson JD, Reynolds M,

WPI; 2000-013248/01.

nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer

Claim 77; Page 79; 148pp; English.

Ð The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endomuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat gnarticularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (

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alterations in phenotype, particularly for identification of therapeutic argets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modification endonucleases are used with DNA). The combination of and/or arctivity. AAA21503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent cestrogen receptor receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA25991 to AAA2617 represent their corresponding target sequences.
                                                                                                                                                                                                                                                                                                          ribozyme sequences and antisense oligonucleotides used in the
                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
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Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;

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Gaps
                                    .
1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
                                0; Indels
                                Conservative
              Local Similarity
hes 16; Conserv
 Query Match
                  Best Loc
Matches
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RESULT 595 AAZ36739/c

AAZ36739 standard; DNA; 17 BP

AAZ36739;

(first entry) 13-MAR-2000

Anchored oligo(dT) primer AT15A used for modified differential display.

88 Stimulus-regulated nucleic acid; sequence profile; nucleic acid level; differentially expressed nucleic acid; disease state; cancer; autoimmune disease; infectious disease, aging; developmental disorder; proliferative disorder; neurological disorder; toxicity; primer; treatment resistance; differential expression; drug discovery; growth factor; epidermal growth factor; radiation; stress; pathogen; se

Synthetic.

W09955913-A2

04-NOV-1999

99WO-US09119. 27-APR-1999;

98US-0083331. 98US-0098070. 99US-0118624. 27-APR-1998; 27-AUG-1998; 04-FEB-1999; (KIMM-) KIMMEL CANCER CENT SIDNEY.

Ë McClelland M, Welsh J,

WPI; 2000-086388/07

Measuring expression of low abundance reduced complexity target nucleic acid molecules -

Example 3; Page 91; 187pp; English.

AAZ36739-41 represent oligo(dT) primers used for modified differential display, in the method of the invention. The specification describes a method for measuring the level of two or more nucleic acid molecules in a target. The method comprises contacting a probe with an arbitrarily or statistically sampled target and detecting the amount of specific binding of the target to the probe. The methods can be used to identify differentially expressed nucleic acid molecules associated with disease states, such as cancer, autolimmune disease, infectious disease, aging, developmental disorder, proliferative disorder or neurological disorder.

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Page 259

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Alternatively the methods can be used to assess the efficacy or toxicity of or a resistance to a treatment. Also the methods can be used to determine differential expression of nucleic acid molecules in response to a stimulus, e.g. a chemical, drug or growth factor (especially epidermal growth factor), radiation, stress or a pathogen. The methods can also be used to determine co-regulated genes that can be potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel nucleic acid molecule comprising a sequence (I) which undergoes significantly low expression in subjects after pollen scattering, and is useful in diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of I cells to the stimulus by an antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gunji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pollinosis-associated gene 441 which undergoes lower expression in subjects after Pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of cells to antigen stimulus
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kashiwabara T, Oshida T, Obayashi M,
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pollinosis; pollinosis-associated gene 441; allergy; T cell;
                                                                                                                                                                Length 17;
                                                                                                                                                                                                0; Indels
                                                                                                                                                               Score 16; DB 1; Le
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pollinosis-associated gene 441 primer #1.
                                                                                                                               Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pollen scattering; antigen; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 35; 42pp; Japanese.
                                                                                                                                                 1.5%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                           17 TAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0148783
                                                                                                  targets for drug discovery.
                                                                                                                                                                                                                                                                                                                                       AAC82874 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2001 (first entry)
                                                                                                                                                                                                                             1083 TAAAAAAAAAAAA
                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOX RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugita Y,
Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-061526/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200073435-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-1999;
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Obayashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2000.
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The invention relates to the human pollinosis-associated gene 787 which exhibits significantly reduced expression in the T-cells of individuals after the pollen-scattering season, relative to expression levels in T-cells before the pollen-scattering season. The gene was isolated from T-cells from individuals allergic to pollen using the differential from Insplay method. The invention also relates to pollinosis-associated gene 787 primers and probes, methods of detection of pollinosis-associated gene 787 nucleic acids, and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 787 nucleic acids. The invention additionally encompasses a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis—sociated gene 787 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 787 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollinosis-associated gene 787 undergoing significantly low expression
in subjects after pollen scattering, useful in diagnosis of allergic
diseases and screening candidate compounds to regulate response of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji
Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E,
                                                                                                                        PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                             Human; pollinosis-associated gene 787; pollen allergy; T-cell;
                                                                                                                                                                             reduced expression; detection; diagnosis; drug screening;
allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Le
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 40; 54pp; Japanese.
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ID AAC92292 standard; DNA; 17 BP.
XX
                    BP.
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                AAC91719 standard; DNA; 17
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to antigen stimulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             GENOX RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                            (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-032159/04.
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                                                                                                                                                                                                                                                                  WO200073440-A1.
                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obayashi I,
                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                     07-DEC-2000.
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagasu T,
                                                   AAC91719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yokoi A;
                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-)
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AAC91719,
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Gaps

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1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels

100.0%; Pr ative 0;

Query Match 1.5 Best Local Similarity 100. Matches 16; Conservative

TAAAAAAAAAAAA 1098

1083

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17 TAAAAAAAAAAAAA

AAC92292

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The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in 6ACG2221), that undergoes significantly low expression in subjects after pollen scattering and is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The present sequence represents a PCR primer which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Pollinosia-associated gene 465 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of reals to antigen stimulus
                                                         Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
                                                                                      Human; pollinosis-associated gene 465; pollen scattering; allergy; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            Kashiwabara T, Oshida T, Obaya
Yoshida N, Ogawa K, Matsui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 43; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; Pre
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                                                                                                                                                                                                                                                     99JP-0148784.
                                                                                                                                                                                                                       18-MAY-2000; 2000WO-JP03191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH47126 standard; DNA; 17
                             (first entry)
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                                                                                                                                                                                                                                                                               (GENO-) GENOX RES INC. (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                          Sugita Y,
Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-061528/07.
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Matches 16; Conserv
                                                                                                                                                              40200073439-A1
                                                                                                                                                                                                                                                     27-MAY-1999;
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                         Nagasu I, S<sup>,</sup>
Obayashi I,
                             22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2001
                                                                                                                                                                                           37-DEC-2000
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Gaps

0

1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0; Indels

1083 TAAAAAAAAAAAA 1098

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16; Conservative

Matches

Query Match Best Local Similarity

17 TARABABABABABA 2

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Obayashi M, Gunji S; ii K, Takahashi E;

The invention provides a method of diagnosis of allergies that involves assaying the levels of expression of genes B1001, B1466, B1072 or B1151 in T-cells; and comparing them with the level of expression in healthy T-cells. The method is useful for diagnosing allergies, particularly atopic dermatitis. The present sequence represents a PCR primer used for analysis of the expression of the above genes.

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Obayashi I, Matsui K,

Oshida T,

Nagasu T,

WPI; 2001-557789/62.

GENOX RES INC. JAPAN GEN NAT CHILDREN'S HOSPITAL.

(GENO-) (NIGE-)

23-FEB-2001; 2001WO-JP01372.

07-SEP-2001

02-MAR-2000; 2000JP-0061832.

Diagnosis of allergies including atopic dermatitis

Example 6; Page 65; 83pp; Japanese

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Examination of allergic diseases comprises detecting gene B1153 over-expressed in T cells of allergy patients for diagnosis treatment and investigation of atopic skin inflammation and asthma
                                                                                                                                                                                                                                                                                                       .;
Ö
                                                                                       Human B1153 expression in allergic disease related PCR primer GT15A.
                                                                                                            Human; allergy; B1153; differential expression; antiallergic; a:
antiasthmatic; antiinflammatory; atopic skin inflammation; PCR;
                                                                                                                                                                                                                                                                                                         Nagasu T,
                                                                                                                                                                                                                                                                                                         Sugita Y,
                                                                                                                                                                                                                                                                      GENOX RES INC.
JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 81; 102pp; Japanese
                                                                                                                                                                                                                                                                                                         Oshida T,
                      BP.
                                                                                                                                                                                                                                                 2000JP-0389476.
                                                                                                                                                                                                                          21-DEC-2001; 2001WO-JP11286
                     AAL49948 standard; DNA; 17
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                         Matsumoto Y, Imai Y,
                                                                                                                                                                                                                                                                                                                              WPI; 2002-713252/77.
                                                                                                                                                                               WO200250269-A1
                                                                                                                                                                                                                                                21-DEC-2000;
                                                                                                                                                         Unidentified
                                                                 LO-DEC-2002
                                                                                                                                                                                                     27-JUN-2002
                                                                                                                                   primer; ss.
                                           AAL49948;
                                                                                                                                                                                                                                                                      (GENO-)
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RESULT 600
         AAL49948/
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Gaps

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B1466; B1072; B1151; T-cell; allergy; atopic dermatitis;

Nucleotide sequence of primer GT15A.

PCR primer; ss.

B1001; human;

WO200165259-A1. Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for examining allergic diseases with intersectin 2 gene or a gene with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is for examining allergic diseases, particularly atopic dermatitis, which is also applicable in screening candidate compounds for remedies, The present sequence is an anchor primer described in the exemplification
The present invention relates to a method of examining allergic diseases which comprises comparing the expression level of gene B1153 in allergy patients with the expression level in healthy subjects. The method is useful for the treatment, prevention, diagnosis and study of allergic diseases including atopic skin inflammation and asthma. The present sequence is a PCR primer described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allergic disease examination method related anchor primer SEQ ID NO: 2.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allergic disease; allergy; antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ή;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for examining allergic diseases by differential display of intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients
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                                                                                                                                                                                Score 16; DB 1; Length 17;
Pred. No. 2.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.5%; Score 16; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagasu T,
                                                                                                                                            Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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                                                                                                                                                                        Query Match 1.3%; Seri Local Similarity 100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                       17 TAAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2000; 2000JP-0314093
                                                                                                                                                                                                                                                                                                                                                                               AAL47234 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hashida R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-372313/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200233122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugita Y, Ha
Takahashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2002.
                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAL47234;
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 8888888888888
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Examining allergosis, involves measuring the expression levels of a specific gene, and comparing it to the levels in the eosinophils of healthy control -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the eosinophils of a healthy person. The method is used for the examination of allergosis. The present sequence represents a PCR primer, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human allergic disease related PCR primer SEQ ID NO: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Le
2.7e+02;
                                                                                                                                                                             Human; allergosis; eosinophil; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                    Nucleotide sequence of PCR primer GT15A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%; Score 16; 00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                         (GENO-) GENOX SOYAKU KENKYUSHO KK.
(KOKU-) KOKURITSU SHONI BYOIN INCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5.,
100.0%; Fi
1083 TAAAAAAAAAAAA 1098
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                      N
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                                                                                                                                                                                                                                                                          25-SEP-2000; 2000JP-0291316
                                                                                ABL59038 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN99829 standard; DNA; 17
                                                                                                                               20-AUG-2002 (first entry)
                       TAAAAAAAAAAAAA
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                                                                                                                                                                                                                            JP2002095500-A.
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                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                    02-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer; ss.
                      17
                                                                                                        ABL59038;
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                                                                      ABL59038,
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The present invention relates to a method for examining allergic diseases which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN99812-ABN99828, in the cosinophils in a patient and comparing the expression level with that in the evainophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for exemplification of the invention.
                                                                                                                                                                                                                                    Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also applicable in screening compounds
                                                                                                        (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                          Example 1; Page 109; 165pp; Japanese.
                                                                                                                                                                Ogawa K,
                                    28-SEP-2001; 2001WO-JP08574
                                                                        13-OCT-2000; 2000JP-0314093
                                                                                                                                                              Sugita Y, Hashida R,
                                                                                                                                                                                                  WPI; 2002-372311/40.
 25-APR-2002
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Saito

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Nagasu

Obayashi M,

Gaps .. 0 1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other; Local Similarity 100. Query Match Matches à

1083 TAAAAAAAAAAAA 1098 17 TAAAAAAAAAAA 2 셤

ABK49634 standard; DNA; 17 ABK49634;

BP.

(first entry) 15-JUL-2002

Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.

Human; 8s; PCR; acetyltransferase; 20-90-05; allergic disease; primer; differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.

Homo sapiens.

WO200224903-A1

28-MAR-2002

25-SEP-2000; 2000JP-0291318

21-SEP-2001; 2001WO-JP08246

(GENO-) GENOX RES INC. (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL. (BISA) EISAI CO LTD.

Nagasu T, Tsujimoto G; Fujishima T, Ogawa K, Hashida R, Takahashi E; Sugita Y,

WPI; 2002-315738/35

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The invention relates to a method for examining allergic diseases comprises determining the expression level of a gene containing, the human offn appearing as ABK49633 which has homology with acetyltransferases in the eosinophils of a patient and comparing the expression level with that in the eosinophils of a healthy individual (i.e. differential display). Also included are methods of screening for candidate compounds which affect the expression level of the gene or the activity of the protein encoded by the gene (including related proteins and mutants), the use of probes based on the gene sequence on the examination of allergic diseases, the use of reporter containing a the transcription-controlling region of the gene, cells transformed with the vector, an antibody against the protein and a model animal for allergic diseases which is a transgenic non-human vertebrate with allergic diseases which is a transgenic non-human vertebrate with the method is examining allergic diseases particularly atopic compounds for remedies. Such method can be performed in high throughput, at low cost. The present sequence is a differential display PCR primer vertebrate and the cDNA encoding the human acetyltransferase-like protein 20-90-05.
                      Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission stage in eosinophils of patients, also applicable in screening
                                                                                                                                                                72pp; Japanese.
                                                                                                         candidate compounds for remedies
                                                                                                                                                        Example 1; Page 56;
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Score 16; DB 1; Length 17; Pred. No. 2.7e+02; 0; Mismatches 0; Indels Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other; 1.5%; Scor 100.0%; Pre Conservative Query Match Best Local Similarity Matches 16; Conserva

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Gaps

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ABK49756 standard; DNA; 17 605

(first entry) 15-JUL-2002

ABK49756;

Human atopic dermatitis cDNA related PCR primer GT15a.

Atopic dermatitis; ss; differential display; primer; PCR; eosinophil; allergic disease; antiallergic; dermatological; GTISa.

Synthetic.

WO200226962-A1.

04-APR-2002

21-SEP-2001; 2001WO-JP08247.

26-SEP-2000; 2000JP-0293021

(GENO-) GENOX RES INC. (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

Nagasu T, Fujishima T, X, Ogawa Hashida R, Sugita Y,

WPI; 2002-330097/36.

Examining allergic diseases by differential display of genes showing different expression particularly increase in remission stage in ecsinophils in patients -

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Gaps

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0; Indels

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21-JUL-2000; 2000GB-0018016.
21-JUL-2000; 2000US-219925P.
                                                                                                                                                        23-JUL-2001; 2001WO-IB01539
                                                                                                                                                                        (GLOB-) GLOBAL GENOMICS AB.
                                                                                                                                                                              Linnarsson S, Ernfors P,
                                                                                                                                                                                    WPI; 2002-217065/27
                                                 of the invention.
                                                                                                                                           WO200208461-A2.
                                                                                                            21-MAY-2002
                                                                                                                                                  31-JAN-2002.
                                                                                                                                      Synthetic.
                                                                                                      ABK13941;
                                                                                                                                                                                                    genes
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having a role in various cellular processes. The method is useful for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present sequence for a PCR primer is used in the production of a single pattern characteristic of a sample, employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus phoenices, for degrading oxalic acid, identifying transformed plant cells, and preventing pathogenic disease in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a primer used in the invention. The invention relates to a novel nucleic acid (see ABZ70560) encoding Aspergillus phoenices oxalate decarboxylase (APOXD) (see ABP72475). The gene and its encoded protein are useful in degrading oxalate, in diagnostic assays, for protecting plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding oxalate decarboxylase from
                                                                                                                                                                                                                                                             1.5%; Score 16; DB 1; Length 17; .00.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxalate decarboxylase; APOXD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 16; DB 1; Le
100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; crop protection; primer; ss.
                                                                                                                                                                                                             Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against disease, and as a selectable marker.
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Best Local Similarity 100."
Matches 16, Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bidney D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Providing mRNA profile, by generating two independent patterns characteristic of sample mRNA population, analysing patterns, comparing gene expression by cell types under varied conditions, and identifying
                                                         This invention relates to gene sequences that are differentially expressed in eosinophils from patients with atopic dermatitis in the increment stage as compared with those in the remission stage. These sequences are used in a novel method to examining allergic diseases comparing the expression levels of these genes and comparing the expression level with that in the eosinophils of a healthy individual. The method of the invention may have antiallergic or dermatological activities. The method can be used to diagnose allergic diseases particularly atopic dermatitis, and may also be used to screen candidate compounds for remedies. The method of the present sequence represents the GTISa PCR primer used to amplify the differentially amplified atopic dermatitis related cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 2.7e+02;
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                   Example 1; Page 54; 74pp; Japanese.
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Best Local Similarity 100.04; Pl
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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases.
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                                                                                                                                                   97JP-0050302.
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                                                                                                                          Sequence derived from the L1 region of the bovine papillomavirus (bPV)
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100.0%; Pred. No. 2.98+02;
cive 0; Mismatches 0; Indels
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                        AAN30173 standard; DNA; 18 BP
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(DANO/) DANOS O.
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         This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases.
                                                                                                                                          Gaps
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                 sequence PCR primer 10.
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Matches 16
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The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
                                                                             Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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                                      Human adipose tissue gene amplifying primer #1
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tes 16; Conserv
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                                                                                                                                    Homo sapiens
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RESULT 612 AAZ90640/c

(NISB) JAPAN TOBACCO

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tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ30631-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity, including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAX96598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
                                                                                                                                       The invention relates to identification of genes and proteins of adipose
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                                                           physiologically active protein specifically derived from mammal
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                        tissue genes.
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                                                                                                                                                                                                                                                                                                                                                 16;
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Length 18;

DB 1;

1.5%; Score 16;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptor-indexers where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method of producing binary sequence
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binary encoded sequence tag; BEST; nucleic acid analysis; gene expression; adaptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 16; DB 1; Length 18;
100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0; Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Latimer DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binary encoded sequence tag method anchored primer
     100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 100; 101pp; English.
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100.0%; Pit
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                                                                                                                                                                                                                                                                                         AAF75596 standard; DNA; 18 BP
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06-APR-2000; 2000US-0544713.
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                                16; Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Gaps

0;

0; Indela

Length 18;

Score 16; DB 1; Le Pred. No. 2.9e+02;

Mismatches

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The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptor-indexers where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes.
                                                                                                                                                                                                                                                                               Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
reverse transcriptase PCR; RT-PCR; primer; ss.
            Binary encoded sequence tag; BEST; nucleic acid analysis; gene expression; adaptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytomegalovirus (HCMV) RT-PCR primer TXN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 100, 101pp; English.
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                                                                                                                                 11-AUG-2000; 2000WO-US22164.
                                                                                                                                                         13-AUG-1999; 99US-0148870.
06-APR-2000; 2000US-0544713.
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                                                                                                                                                                                                                                                                                                                         and adaptor-indexers
                                                                                                                                                                                                                                                     WPI; 2001-202878/20.
                                                                                                                                                                                                 (UYYA ) UNIV YALE
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                                                                                                     22-FEB-2001
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                                                    Synthetic
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The present invention relates to a new method for identifying compounds related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, Rinses Compound with at least one of the cellular kinases RICK, RIP, Rinses RICK-Interacting kinase, MKK3 and SREK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CNV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present nucleic acid sequence represents human CMV reverse transcriptase (RT)-PCR primer TXN that was used in the methods of the invention for preparation of radioactively labelled cDNA probes.
                                                                                                                                                         infection, comprises contacting test compound with cellular kinase and detecting change in cellular kinase activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Providing mRNA profile, by generating two independent patterns characteristic of sample mRNA population, analysing patterns, comparing gene expression by cell types under varied conditions, and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                     Identifying agents for treatment or prevention of
                                                                                                Stein-Gerlach M,
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                                                                                                                                                                                                                 Example 1; Page 13; 49pp; English.
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15-OCT-2001; 2001EP-0124604.
                              16-OCT-2000; 2000US-240750P.
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21-JUL-2000; 2000US-219925P.
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Best Local Similarity 100."
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                                                            (AXXI-) AXXIMA PHARM AG
                                                                                                                        WPI; 2002-373930/41
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                                                                                           Schubart D,
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Gaps

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Length 18; 0; Indels

1.5%; Score 16; DB 1; De 100.0%; Pred. No. 2.9e+02; live 0; Mismatches 0;

/note= "n= dATP, dCTP or dGTP"

/*tag= a /label= n

Location/Qualifiers

(first entry)

Latimer DR;

ij Feng

Lizardi PM,

Roth ME,

0

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Homo sapiens
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XX
AC
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AADS;
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CHR;
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mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present sequence for characteristic forms in the production of a single pattern.
                                                                                  The present invention relates to a method for providing a profile of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characteristic of a sample, employing a Type II restriction enzyme (i.e. HaeII) in the methods of the present invention.
Disclosure; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characteristic
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Gaps . Score 16; DB 1; Length 18; Pred. No. 2.9e+02; 0; Indels Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 other; Query Match
Best Local Similarity 100.0%; Pred. Mc. -Matches 16; Conservative 0; Mismatches

AAAAAAAAAAAAA 1

AAD52799 standard; DNA; 18

Primer used to prepare radioactively labelled cDNA probes from RNA. 14-MAY-2003 (first entry)

Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie; cellular protein phosphatase; cellular signal transduction; prophylaxis; prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease; CJD; transmissible mink encephalogathy; bovine spongiform encephalopathy; TWE; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome; fatal familial insomnia; FPI; kuru; neurodegenerative disease; nootropic; Alzheimer's disease; primer; ss.

WO200293164-A2.

16-MAY-2002; 2002WO-EP05420,

16-MAY-2001; 2001EP-0111858. 29-MAY-2001; 2001US-293528P. 13-JUL-2001; 2001EP-0117113. 13-JUL-2001; 2001EP-0117113. 18-JUL-2001; 2001US-305898P.

(AXXI-) AXXIMA PHARM AG

Mueller S; Bacher G, Stein-Gerlach M, Salassidis K,

WPI; 2003-120714/11.

New pyridylpyrimidine derivatives useful in the treatment or prevention of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease

Example; Page 38; 96pp; English.

The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells, cell cultures and/or cell lysates. The method involves adding at least one monoclonal or polyclonal antibody, oligonucleotide or pyridyleast one monoclonal or polyclonal antibody, oligonucleotide or pyridylysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-R1 (also known as flg, F1-1, F1t-2, b-FGFR), rk (also known as CCK-2, DDR-2 or BDDR, BC number 2.7.1.112), Abl (also known as CCK-1), PRK), human cellular protein phosphatases such as prp-SL cknown as CDK1), PRK), human cellular protein phosphatases such as prp-SL conjection as GPR ond GPIR-1. The invention is useful for regulating the composition for prophylaxis and/or treatment of infectious disease (e.g. production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. TMB), Creutzfeldt-Jacob disease (CMD), transmissible mink encephalopathy (BSB), variant CJD, deretmann-Straussler-Scheinker syndrome (GSS), fatal cortinains (FRI), Kuru and Alpers syndrome, especially BSE, CJD, or ruminants. The present DNA sequence is a primer used to prepare composition of the invention. 886666666666666666666668888

Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

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Gaps . 0 Score 16; DB 1; Length 18; Pred. No. 2.98+02; 0; Mismatches 0; Indels 1.5%; Scc. 100.0%; Pred. No. ... 16; Conservative Local Similarity Matches

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à 엄

AAS05714 standard; DNA; 20 RESULT 620 AAS05714

ВЪ

(first entry) 07-SEP-2001 AAS05714;

Aminopurine substituted region of an RP-TFO.

reverse phase triplex forming oligonuclectide; RP-TFO; protected nucleic acid sequence; PNAS; single nuclectide polymorphism; SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.

Synthetic,

/*tag= b /label= "OTHER" /note= "A is aminopurine substituted" 'note= "A is aminopurine substituted" /label= "OTHER" /note= "A is aminopurine substituted' Location/Qualifiers C"OTHER" /*tag≈ a /label= "OTHER" *tag= d label= OTHER *tag= *tag= Key modified_base modified_base modified_base Modified base

"A is aminopurine substituted" 'note= "A is aminopurine substituted' /*tag= f /label= "OTHER" note= modified base modified base

/*tag=

note= "A is aminopurine substituted"

/label= "OTHER"

'note= "A is aminopurine substituted"

*tag= g |abel= "OTHER"

*tag=

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Sequence 20 BP; 19 A; 0 C; 0 G; 0 U; 1 other;
                                                                                                                                                                                                                                  Example 2; Page 66; 141pp; English.
                                                                                                                                                        03-NOV-1999; 99US-0163356.
03-NOV-1999; 99US-0163416.
21-DEC-1999; 99US-0171348.
07-UUL-2000; 2000US-0216579.
                                                                                                                                              03-NOV-2000; 2000WO-US30534.
                                                                                                                                                                                             Oste CC, Ramberg ER;
                                                                                                                                                                                                      WPI; 2001-343488/36.
                                                                                                                                                                               (CYGE-) CYGENE INC. (OSTE/) OSTE C C.
                                                                                                                             WO200132929-A1
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'note= "Other= Hypoxanthine or Inosine

J "OTHER"

/*tag= _ /label= '

'note= "A is aminopurine substituted"

/*tag= l /label= "OTHER"

'note= "A is aminopurine substituted"

'*tag= k 'label= "OTHER"

*tag= i |label= "OTHER" |note= "A is aminopurine substituted"

note= "A is aminopurine sustituted"

*tag= h label= "OTHER"

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This invention describes a novel recognition system comprising at least I recognition unit bound to a support, each recognition unit comprising region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids and/or proteins, and for screening for and/or peptides, nucleic acids, chemical agents, preferably proteins, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure.
                                                                                                                                                                                                                                                                       Recognition system; screening; identification; pharmaceutical; toxin; plant protection agent; toxin; venom; carcinogen; venom; teratogen; herbicide; fungicide; pesticide; beta-actin; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T7T18Apad_PS27-20-0003 probe for calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 16; DB 1; Length 20; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 2 A; 2 C; 2 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgstaller P;
                                                                                                                                                                                                                             Human S-9 derived oligonucleotide #7.
                                                                                                        BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examples; Fig 1; 8pp; German.
  AAAAAAAAAAAAA 16
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                                                                                                    AAC82923 standard; DNA; 20
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Best Local Similarity 100.00
These 16; Conservative
                                                                                                                                                                                      21-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                DE19923966-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is a second reverse phase triplex forming oligonucleotide, RP-TRO (3' to the SNP) used to analyse Factor V Leiden SNP using the method of the invention. The invention relates to analysing target uncleic acid sequences comprising restricting isolated DNA, hybridising target nucleic acid sequences comprising restricting isolated DNA, hybridising car least one triplex forming oligonucleotide (TFO), adding a 3 to 5' exponuclease to form a protected nucleic acid sequence (PNAS) tail of structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, short tandem repeats (STRS). The methods can be used to detect SNPs for use in population genetics, drug development, forensics, cancer, genetic contains, plants and animals.
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in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonucleotide and probe to target sequence -
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0

Gaps 0;

Query Match
1.5%; Score 16; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0;

0; Indels

Delenstarr GC;

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The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating acts of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
PCR primer; ss.
                                                                                                                                                                                                                                           Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                  Disclosure, Page 14; 32pp; English.
                                                                                                                                                          (AGIL-) AGILENT TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA05917 standard; DNA; 20 BP
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                                                                                                   10-SEP-2001; 2001EP-0307665.
                                                                                                                                11-SEP-2000; 2000US-0659173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                   WPI; 2002-282886/33.
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                                                                                                                                                                                                                                                                                          calibration probes
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                Unidentified
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                                        EP1186673-A2
                                                                       13-MAR-2002.
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This invention descibes a novel method for the analysis of a DNA fragment which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment. (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence to the above mentioned known common oligonucleotide sequence, a second common primer containing a complementary nucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with common oligonucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the gene having known sequence, to give amplified DNA, (iii) analysis of the amplified DNA to find the information of the DNA fragment, in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation.
                                                                                                                               The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of lift is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention.
              Diagnosing hepatitis B virus (HBV) infection stages and determining trisk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer; DNA analysis; amplification; hybridisation; ss.
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Local Similarity 100.0%; Pred. No. 3.2e+02;
les 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide 8 for DNA analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 12; 17pp; Japanese
                                                                                             Example 1; Page 6; 25pp; English.
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Score 16; DB 1; Length 20; Pred. No. 3.2e+02; 0; Mismatches 0; Indels

100.0%; Pre

(first entry)

Koike K;

1.5%;

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RESULT 626
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Differentiation of informations of known and unknown genes readily provides information of unknown gene and simultaneous monitoring of signals derived from minor genes. Furthermore, labelling of DNAs according to functions of Known genes can be performed. AAZ09189-209201 represent oligonucleotide primers used to illustrate the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different scanned from anolecular array, or calibrating different scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data.
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                      T7T18Apad_PS26-21-0003 probe for calibration of molecular array data.
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                                                                                                            1.5%; Score 16; DB 1; Length 21;
100.0%; Pred. No. 3.48+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0; Indels
                                                                                 Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 32pp; English.
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                                                                                                                                                                                                                                                AAD33500 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                              Molecular array; probe; ss.
                                                                                                        Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-282886/33.
                                                              the invention
                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                              01-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from anolecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly normalisation probe used in calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of
                                                                                                                                T7T18Apad_PS25-22-0003 probe for calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleavase, Thermus,
Mycobacterium; Shigella,
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 16; DB 1; Length 22;
100.0%; Pred. No. 3.58+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 16 A; 4 C; 0 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p53; mutant; mutation; cleavage; nuclease;
Escherichia; Saccharomyces; Campylobacter;
Staphylococcus; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer for tyrosinase gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGIL-) AGILENT TECHNOLOGIES INC.
         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 AAAAAAAAAAAA 1099
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                                                                                                                                                                                                                                                                                                                                                               10-SEP-2001; 2001EP-0307665.
                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000; 2000US-0659173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAAAAAAAA 16
AAD33501 standard; DNA; 22
                                                                                                                                                                              Molecular array; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT29081 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delenstarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-282886/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calibration probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 16; Conserv
                                                                                      01-JUL-2002
                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                    EP1186673-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wobler PK,
                                              AAD33501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT29081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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Gaps

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1084 AAAAAAAAAAAA 1099

Conservative

Local Similarity

Best Loc Matches

WO9615267-A1

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The present sequence represents a specifically claimed oligonucleotide PCR primer. The oligonucleotide can be used for polymerase chain reaction (PCR) amplification of DNA, specifically regions of specific genes that are conserved among mammalian species, i.e. pairs of oligonucleotides from the present specification represent universal mammalian sequence-tagged site (UM-STS) primers. The primers are used to develop genomic maps, to include clones from libraries, to make cross-species comparisons and to develop additional genetic marker. UM-STS allow genomic comparisons to be made between more species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer; ss, liver regeneration, gene panel; expression profile, screening, drug development; hepatitis; liver transplantation.
                                                                                                                                                                                                                 New oligonucleotide primers amplifying gene regions conserved amono
mammals - useful for developing genomic maps, isolating clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahara Y, Fukuda H, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liver regeneration-related gene panel PCR primer #115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Score 15.8; DB 1;
89.5%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
                                                                                                                                      Yuzbasiyan-Gurkan V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                          making cross-species comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTTGGGGGCTGCAGC 154
                                                                                                                                                                                                                                                                                              Claim 1; Page 9; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okutsu I, Mori M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 crecriraccecrecaec
97WO-US02403.
                                       96US-0012061.
                                                                        (UNMI ) UNIV MICHIGAN. (UNMS ) UNIV MICHIGAN STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2002; 2002WO-JP02372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001; 2001JP-0070940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABT13587 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 89.5 es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AJIN ) AJINOMOTO CO INC.
                                                                                                                                      Venta PJ,
                                                                                                                                                                            WPI; 1997-435083/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-018922/01.
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18-FEB-1997;
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                                                                                                                                    Brewer GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002.
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Sonaka I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABT13587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RIM) BN enzyme, C Thermus aquaticus DNA polymerase. Thermus thermophilus DNA polymerase. Escherichia coll ExoIII and the Saccharomyces cerevisiae polymerase, Becherichia coll ExoIII and the Saccharomyces cerevisiae and I/O complex. The nucleic acid substrate is preferably an alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses. The human tyrosinase gene (both wild type and mutant gene fragments) was used as a test sequence for the method. Three primers (AAT22069-82) were used alongside other primers (AAT27689-90) and in combination, to amplify fragments of wild type and mutant tyrosinase genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                       Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer; polymerase chain reaction; amplification; UM-STS; universal mammalian sequence tagged site; genomic map; clone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                Fors L, Heisler LM, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 15.8; DB 1; Length 189.5%; Pred. No. 3.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elastin PCR primer for universal mammalian STS's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 3 A; 2 C; 7 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10; Page 119; 433pp; English.
                                                                                                                                                                                                    (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 GCCAGTTTGGCATTTGGGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCAAGTTTGGCTTTTGGGA 19
                                                                                                                        94US-0337164.
95US-0402601.
95US-0484956.
                                                                  95WO-US14673.
                                                                                                     95US-0520946.
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                                                                                                                                                                                                                                            Brow MAD, Dahlberg JE,
Oldenburg MC, Olive DM,
                                                                                                                                                                                                                                                                                                    WPI; 1996-259862/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                            09-NOV-1995;
                                                                                                                          09-NOV-1994;
                                                                                                                                        09-MAR-1995;
                      23-MAY-1996
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                                                                                                                                                                                                                                          Brow MAD,
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Query Match

Matches

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Gaps

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Length 19; Indels Gene panel participating in liver regeneration, applicable in providing expression data, diagnosis and development of drugs for promoting liver regeneration e.g. after transplantation or removal of liver during

cancer

WO9731012-A1 28-AUG-1997.

Synthetic.

AAV01125;

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Gaps

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Score 15.8; DB 1; Length 19; Pred. No. 3.3e+02; 0; Mismatches 2; Indels

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The invention comprises a gene panel constructed from the expression profile of known genes which show a change in expression level between normal liver cells and liver cells under regeneration. The gene panel is useful for providing expression data and screening/development of drugs for liver regeneration (e.g. when treating hepatitis, after transplantation or removal of the liver during cancer or hepatitis threapy). The present DNA sequence represents a PCR primer used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calpain; subunit; calcium; protease; mutation; treatment; detection; identification; diagnosis; limg girdle muscular dystrophy; LGMD2; calcium activated neutral protease; CANP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The calpain large subunit I gene located on chromosome 15 codes for a calcium activated neutral protease (CANP3) belonging to the calpain family. Mutations in the gene induce limb-girdle muscular dystrophy (LGMD) 2 disease. The gene, and fragments of it, can be bredisposition to LGMD2 treatment, diagnosis and detection of a predisposition to LGMD2 disease. Fifty primers (AAT32510-59) were used to specifically amplify the exons and splice junctions of the calpain large subunit I gene as well as the regions containing the putative CAT, TATA boxes and the polyadenylation signal. Two primers (AAT32534, AAT32535) were used to amplify exon 12 of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel Calpain large sub:unit 1 gene encoding a calcium dependent protease - used to develop prods. for the diagnosis treatment of limb-girdle muscular dystrophy 2 disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer for exon 12 of the calpain large subunit 1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 1 C; 12 G; 4 T; 0 other;
                                                                                                                                                                                                Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 other;
Claim 19; Page 76; 101pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASFR-) ASSOC FR CONTRE MYOPATHIES.
                                                                                                                                                                                                                                                                                                     761 GATGGCAGAACTGGAGAAG 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 13; 66pp; English.
                                                                                                                                                                                                                                 1.4%;
89.5%;
                                                                                                                                                                                                                                                                                                                                        GATTGCAGAACTGGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-EP04575
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                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           AAT32535 standard; DNA;
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel antisense oligonucleotides (OGNS) (I) 88-20 nucleotides in length that specifically hybridize with and inhibit nucleic acids encoding human Fas-associated death domain (FADD), targeted to the 3' untranslated region (3'UTR). (I) can be used to treat animals, especially humans, suspected of having or being prone to a disease or condition associated with FADD expression. AAZ44746-Z44831 represent primers and probes used in the method of the invention.
                                                                                                                                                                                                                      FADD; human; antisense; inhibitor; Fas-associated death domain; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotides, useful for inhibiting human Fas-associated death domain (FADD) expression are targeted to the 3' untranslated region of the FADD gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reverse phase triplex forming oligonucleotide, RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
      Gaps
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      Indels
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    2,
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 other;
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang
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                         394 GCACACACCCCTGCTCCA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GGCCGTGGCTCAGCTCTTG 251
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                                                                                                                                                                                              Human FADD primer ISIS #101866
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                                              GCACACTCACCCTCCTCCA
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Local Similarity 89.5%;
les 17; Conservative
                                                                                                                  AAZ44829 standard; DNA; 20
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                                                                                                                                                                    19-APR-2000 (first entry)
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-126316/11
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                         19-JUL-1999;
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17;
                                                                                                                                                                                                                                                                                      US6015712-A.
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                                                   20
                                                                                                                                            AAZ44829;
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                                                                                                                                                                                                                                     probe;
                                                                                         RESULT 631
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Matches
Matches
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                                                                                                      AAZ44829,
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Length 20;

Score 15.8; DB 1; Pred. No. 3.5e+02;

1.4%;

Query Match Best Local Similarity

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The sequence is a polypyrimidine oligonucleotide for binding a second reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to the target SNP used to analyse Factor V Leaden SNP using the method of the invention. The invention relates to analysing target nethod of the invention. The invention relates to analysing target at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exomuclease to form a protected incleic acid sequence (PNAS) tail structure, hybridising the captured structure with a single nucleotide structure, hybridising the captured structure with a single nucleotide collymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeate (STRS). The methods can be used to detect SNPs or use in population genetics, drug development, forensies, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in humans, plants and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonucleotide and probe to target sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemoglobinopathy, sickle cell anaemia; haemoglobin; beta-globin;
HbS; HbA; gene therapy; triple helix; triplex; psoralen; mutagen;
targeted DNA replacement; TDR; homologous recombination; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Third-strand oligonucleotide pyrimidine/parallel motif for TDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 15.8; DB 1; Length 20; llarity 89.5%; Pred. No. 3.5e+02; Conservative 0; Mismatches 2; Indels
   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key Location/Qualifiers misc difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 66; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 ATTABABABABABABA 1099
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                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1999; 99US-0163416.
21-DEC-1999; 99US-0171348.
07-JUL-2000; 2000US-0216579.
                                                                                                                                                                                                                                                                             03-NOV-2000; 2000WO-US30534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT48469 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oste CC, Ramberg ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-343488/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CYGE-) CYGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OSTE/) OSTE C C.
                                                                                                                                     WO200132929-A1
                                                                                                                                                                                                                                                                                                                                                    03-NOV-1999;
                                                                                                                                                                                                           10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT48469;
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Matches
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Indels

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Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premaliann metaplastic lesion; endometriosis; dysplastic lesion; benign tumnour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                 Third-strand oligonucleotides (AAT48467-70) bind to a purine-rich region (see also AAT48455) located at position 2655 in the beta-globin gene (see also AAT48454). They can be utilised in a targetted DNA replacement (TDR) method to correct a mutation that leads to sickle cell anaemia. In TDR, a third-strand oligonucleotide is targetted to a binding region in the gene, where it induces DNA damage. This stimulates homologous recombination with an introduced donor nucleic acid strand. TDR is highly specific and, since the corrected gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                           Repairing mutation(s) in haemoglobin by targetted mutagenesis or homologous recombination - mediated by a triplex forming oligonuclectide, opt. carrying a mutagen, partic. for treatment of sickle cell anaemia or thalassemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 15.8; DB 1; Length 21; 89.5%; Pred. No. 3.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism; human; inhibitor; cancer; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is in its native chromosome, the cure is permanent
 /*tag= a
/note= "psoralen attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 47; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AAGAAACGGGAAGAAAGGA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polymorphic region 821.
                                                                                                                                     95US-0473845
                                                                                                        96WO-US09430
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                              WPI; 1997-099895/09.
                                                                                                                                                                 (UYYA ) UNIV YALE.
                                                                                                        06-JUN-1996;
                                                                                                                                     07-JUN-1995;
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                                                                          19-DEC-1996
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                                                                                                                                                                                                 Glazer PM
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Stanton VP;

Ledley FD,

potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for call growth or viability, and where the gene is subject to loss of heteroxygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient having a precancerous condition, by administering to the patient having a present in cells of the precancerous condition, where the normal somatic cells of the patient are heteroxygous for the first gene, the inhibitor of a active on at least one but less than all allelic forms of the gene or present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can commal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, dysplastic lesions, benign tumours, endometricosis, polycyptic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z26825 crementic. Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometricsis or graft versus host disease invention describes a novel method for identifying an inhibitor Disclosure; Figure 7; 605pp; English WPI; 1998-521232/44. Housman D,

; 1.4%; Score 15.8; DB 1; Length 21; 89.5%; Pred. No. 3.6e+02; tive 0; Mismatches 2; Indels 2; Indels Sequence 21 BP; 15 A; 2 C; 1 G; 3 T; 0 other; 1081 ATTABABABABABABA 1099 3 ATTAACTAAAAAAAAA 21 Local Similarity 89.5 Query Match Matches ð g

AAX14729 standard; DNA; 21 BP. AAX14729; RESULT 635 AAX14729/C
XX
AC AAX1XX
AC AAX1XX
DT 24-M
XX
DE Trip
XX
DE Tri

(first entry) 24-MAR-1999

Triple helix third strand of Beta-globin gene nucleotides 742-762.

detection; triple helix; identification; bacteria; oncogene; virus; ss. DNA Triplex formation;

Synthetic. Homo sapiens

US5861244-A 19-JAN-1999 93US-0173489. 22-DEC-1993;

92US-0968436. 93US-0173489 22-DEC-1993; 29-OCT-1992; (PROF-) PROFILE DIAGNOSTIC SCI INC.

Hepburn AG, Wang C;

WPI; 1999-130384/11

Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria

Disclosure; Columns 17-18; 168pp; English.

The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the sequence it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded by test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for the method is used to detect DNA sequences, particularly for clientification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.

21 BP; 0 A; 7 C; 0 G; 14 T; 0 other; Sequence

Gaps ., Length 21; Local Similarity 89.5 1es 17; Conservative Query Match Matches

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à g

AAZ27844 standard; DNA; 22 AAZ27844; RESULT 636 AAZ27844/

.; 0

Gaps

23-DEC-1999 (first entry)

PCR primer for human DNA marker clone S103.

Tandem repeat sequence; DNA isolation; intermediate tandem repeat; TR sequence; pentanuclectide tandem repeat; stutter artifact; DNA typing; DNA profiling; linkage analysis; criminal justice; paternity testing; animal lineage analysis; microsatellite loci; polymorphism detection; PCR primer; ss.

Synthetic

Homo sapiens

WO9940194-A1.

12-AUG-1999

99WO-US02345. 04-FEB-1999; 04-FEB-1998;

98US-0018584.

(PROM-) PROMEGA CORP.

Bacher JW; Schumm JW, WPI; 1999-590696/50.

DNA containing intermediate tandem repeat sequences, in DNA profiling Isolating

Claim 30; Page 22; 111pp; English.

This sequence is a PCR primer for a human DNA marker clone used in the

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method of the invention. The method is for isolating a fragment of DNA containing an intermediate tandem repeat (ITR) sequence using hybridization selection, and comprises: (a) providing several DNA fragments at least one of which contains an ITR sequence, a region of the DNA fragment which contains an ITR sequence, a region of the DNA fragment which contains a ITR sequence, a region of times; (b) providing a stationary support having at least two climes; (b) providing a stationary support having at least one oligonuclectide associated with it, where the oligonuclectide includes a sequence; and (c) combining the DNA fragments with the support under conditions where the DNA fragments including the DNA fragment containing used to isolate DNA containing pentanuclectide tandem repeat sequences as well as to detect target ITR DNA sequences having a low incidence of souther artifacts (no more than 2.4%). The method is useful in DNA profiling for linkage analysis, criminal justice, paternity testing and other forensic and medical uses. DNA typing is also useful for confirming the lineage of horses, dogs and other prize animals. The invention of constitution when method on the use of microsatellity of in DNA profiling 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electrophoretic gels. This allows the simultaneous analysis of more loci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          profiling. The method can detect polymorphisms with a low incidence of stutter artifacts, which has previously been a problem in interpreting allelic content of loci. The development of markers based on larger repeat units, enables easier separation of the fragments on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis; nucleic acid detection; nanostructure; biochip; biofilter; drug delivery; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 2 A; 12 C; 2 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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2000US-255235P.
2001US-0760500.
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28-MAR-2001; 2001US-0820279.
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2000US-213906P.
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Park S, Li Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656926/75.
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26-JUN-2000;
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The invention relates to a method for detection of nucleic acid (I)

having at least 2 portions, comprising treatment with nanoparticles that

carry oligonucleotides complementary to at least 2 parts of (I), where

detectable change caused by hybridisation of the oligonucleotide to (I)

is observed. The method is used to detect (or to separate) specific (I),

e.g. for diagnosing a wide variety of diseases, sequencing, in forensic

analysis etc., and generally to detect analyses other than (I). The

cligonucleotide-derivatised nanoparticles are also useful for preparing

nanostructures useful, for example, as biochips, biofilters, mechanical

devices, separation membranes, chemical sensors, in computers, and for

drug delivery. Very stable nanoparticle-oligonucleotide conjugates

can be produced, allowing their direct use (as probes) in polymerase

can be produced after amplification. (I) are detected by simple

colour change, without the need for special equipment, making possible

rapid field testing for e.g. pathogens. AAS631374-AAS63448 represent

colour change, has invariable probes, and related sequences, used in the

mathod of the advance of the colour probes, and related sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonuclectide-nanoparticle probe; diagnostic; forensic analysis; nucleic acid detection; nanostructure; biochip; biofilter;
               Detecting and separating nucleic acid, useful e.g. for diagnosis, comprises reaction with nanoparticles that carry oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucic RC, Storhoff JJ, Elghanian R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 15.8; DB 1; Length 2
89.5%; Pred. No. 3.8e+02;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide-nanoparticle probe #43.
                                                                                       Example 16; Page 139; 404pp; English.
                                                      complementary to parts of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1076 CAACTATTAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CAACTCGTAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS63419 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2000; 2000US-192699P.
26-APR-2000; 2000US-200161P.
26-JUN-2000; 2000US-213906P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2000; 2000US-0603830.
08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255235P.
12-AN-2001; 2001US-0760500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001WO-US10071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2001; 2001US-0820279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mirkin CA, Letsinger RL,
Taton TA, Park S, Li Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 89.5
                                                                                                                                                                                                                                                                                                                                                                                                                                             method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug delivery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200173123-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS63419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 638
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The invention relates to a method for detection of nucleic acid (I) having at least 2 portions, comprising treatment with nanoparticles that carry oligonucleotides complementary to at least 2 parts of (I), where caused by hybridisation of the oligonucleotide to (I) is observed. The method is used to detect (or to separate) specific (I), e.g. for diagnosing a wide variety of diseases, sequencing, in forensic analysis etc., and generally to detect analyses other than (I). The oligonucleotide-derivatised nanoparticles are also useful for preparing nanostructures useful, for example, as biochips, biofilters, mechanical devices, separation membranes, chemical sensors, in computers, and for devig delivery. Very stable nanoparticle-oligonucleotide conjugates can be produced, allowing their direct use (as probes) in polymerase chain reaction, ie. they survive multiple heating/cooling cycles so do not need to be added after amplification. (I) are detected by simple colour change, without the need for special equipment, making possible rapid field testing for e.g. pathogens. AAS63174-AAS63448 represent coligonucleotide-nanoparticle probes, and related sequences, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nanoparticle, oligonucleotide, DNA detection, DNA isolation, genetic disease, bacterial disease, viral disease, forensic science, paternity testing, gene therapy, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "C is covalently linked to a colloidal gold
particle via a HS(CH2)3 moiety"
                                 Detecting and separating nucleic acid, useful e.g. for diagnosis, comprises reaction with nanoparticles that carry oligonucleotides complementary to parts of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/bound_moiety= "Nucleotides 12-1 of the sequence
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 1; Length 22;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide-gold conjugate, capture oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                       Example 17; Figure 26B; 404pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CAACTCGTAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS10359 standard; DNA; 22 BP
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26-APR-2000; 2000US-0200161.
26-JUN-2000; 2000US-0603830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-2001; 2001WO-US01190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      method of the invention.
 WPI; 2001-656926/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200151665-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS10359,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The sequence represents an oligomucleotide which is linked by its 3' end to a nanoparticle. The sequence is complimentary to a target oligomucleotide. The nanoparticle may be linked to several oligomucleotides. The nanoparticle may be linked to several oligomucleotides. The sequence is used to demonstrate the method of the invention. The invention relates to isolating or detecting a moleic acid finterset, in a mixture of mucleic acids, by binding it to 2 or more complimentary nuclectides which have a nanoparticle attached to their 5' ends. The nanoparticles (e.g. colloidal gold) are used to both isolate complimentary nuclectides which have a nanoparticle attached to their 5' ends. The manoparticles (e.g. colloidal gold) are used to both isolate or and detect (e.g. by linking the particle to a fluorescent probe) the resultant complex. The methods are useful for detecting nucleic acids, natural or synthetic, and modified or unmodified. The methods may also be applied in the diagnosis of genetic, bacterial and viral diseases, in for monitoring gene therapy. The methods are further useful in research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens; cor quick identification of an infection to assist in drug prescription, and in homes and health centres for inexpensive (irst-line screening. The methods, which are based on observing classified and little or no instrumentation; and ill homes and the surface specialised or expensive equipment, and little or no instruments of require specialised or expensive equipment, and little or no instruments.
                                                                                                                                                                                                                                                                                                      Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or viral diseases, by contacting the nucleic acid with oligonucleotides attached to nanoparticles and having sequences complementary a portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nanoparticle, oligonuclectide; DNA detection; DNA isolation;
genetic disease; bacterial disease; viral disease; forensic science;
paternity testing; gene therapy; ss.
                                                                                                                                               Storhoff JJ, Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/bound_moiety= "Nucleotides 12-1 of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide-gold conjugate, capture oligonucleotide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   instrumentation is required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         appearing as AAS010364"
                                                                                                                                               Mucic RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 16; Page 110; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
12-JAN-2001; 2001US-0760500.
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                                                                                                                                        Letsinger RL,
Li Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 89.5
                                                                    (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                         WPI; 2001-451868/48.
                                                                                                                                                                                                                                                                                                                                                                                                              of the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and little or no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
misc_binding
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                                                                                                                                        ą,
                                                                                                                                    Mirkin CA,
Taton TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS10362;
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Matches
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NAMES OF THE STATE OF THE STATE
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The sequence represents an oligomuclectide which is linked by its 3' end to a nanoparticle. The sequence is complimentary to a target of to a nanoparticle. The sequence is complimentary to a target oligomuclectides. The nanoparticle may be linked to several oligomuclectides. The nanoparticle may be linked to several twention. The invention relates to isolating or detecting a nucleic acid of interest, in a mixture of mucleic acids, by binding it to 2 or more complimentary nuclectides which have a nanoparticle attached to their 5' ends. The nanoparticles (e.g. colloidal gold) are used to both isolate complimentary nuclectides which have a nanoparticle attached to their 5' and detect (e.g. by linking the particle to a fluorescent probe) the cresultant complex. The methods are useful for detecting nucleic acids, natural or synthetic, and modified or unmodified. The methods may also be complied in the diagnosis of genetic, bacterial and viral diseases, in formatication, and for monitoring gene therapy. The methods are uthentication, in the field to detect the presence of specific pathogens, sequencing, in the field to detect the presence of specific pathogens, or prescription, and in homes and health centres for inexpensive colour change with the naked eye, are cheap, fast, simple, robust and little or no instrumentation is require specialised or expensive equipment, and illetine mand the properties of an infection to assist in drug
                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or viral diseases, by contacting the nucleic acid with oligonucleotides attached to nanoparticles and having sequences complementary a portion of the nucleic acid.
/note= "A is covalently linked to a colloidal gold
particle"
                                                                                                                                                                                                                                                                                                                                Mucic RC, Storhoff JJ, Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Score 15.8; DB 1; Length 22; 89.5%; Pred. No. 3.8e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and little or no instrumentation is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Random oligonucleotide, SEQ ID NO: 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Fig 23; 323pp; English.
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                                                                                                                                                                                                         26-APR-2000; 2000US-0200161.
26-UUN-2000; 2000US-0603830.
12-UAN-2001; 2001US-0760500.
                                                                                                                                                   12-JAN-2001; 2001WO-US01190.
                                                                                                                                                                                           2000US-0176409.
                                                                                                                                                                                                                                                                                                                                Letsinger RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF28471 standard; DNA;
                                                                                                                                                                                                                                                                                         (NANO-) NANOSPHERE INC
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-451868/48.
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                                                                         40200151665-A2
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                                                                                                                                                                                           13-JAN-2000;
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                                                                                                              19-JUL-2001
                                                                                                                                                                                                                                                                                                                              Mirkin CA,
Taton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF28471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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              ##X8X8X8###X4X###X#X####X#X#X#X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an oligonucleotide used in a method for detecting a nucleic acid having at least 2 portions. The method comprises hybridising the nucleic acid with Oligonucleotides, such as the present sequence, attached to a substrate and/or particle and detecting a change in colour, conductivity or optical density. The method is useful for the diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing, for paternity testing, for cell line authentication and for monitoring gene therapy. Detecting nucleic acids based upon observing a colour change is cheap, fast, simple, and does not require specialised or expensive equipment. The nanoparticle oligonucleotide conjugates remain stable for at least 6 months. A single base mismatch and as little as 20 femtomoles (fM) of target can be detected using the conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
cell line authentication; gene therapy; ss.
disease diagnosis; forensic analysis; DNA sequencing; patexnity testing; cell line authentication; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics and DNA sequencing, comprises observing detectable change brought about by hybridization of nucleic acid with substrate or
                                                                                                                                                                                                                                                                                                                                     Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 15.8; DB 1; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                  Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; 2-
3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Random oligonucleotide, SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 16; Page 85; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1076 CAACTATTAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                              particle bound oligonucleotides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CAACTCGTAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВЪ
                                                                                                                                                                      25-JUN-1999; 99US-0344667.
26-APR-2000; 2000US-0200161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.5%;
                                                                                                                                         26-JUN-2000; 2000WO-US17507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF28474 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                    LETSINGER R L.
MUCIC R C.
STORHOFF J J.
BLGHANIAN R.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-061976/07.
                                                                                                                                                                                                                      (MIRK/) MIRKIN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                  (ELGH/) ELGHANIAN (TATO/) TATON T A.
                                                                             WO200100876-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2001
                                                                                                             04-JAN-2001
                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                  Taton TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF28474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                     (LETS/)
(MUCI/)
(STOR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF28474
ਨੇ
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Synthetic.

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Gaps

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The invention discloses methods for removing silver from a silver stained DNA detection chip having bound gold nanoparticles, which comprises using ac oyanide etching solution or ultrasound waves. The chip based DNA detection method employs gold nanoparticle probes, modified with comprises to indicate the presence of a particular DNA sequence of igonuclectides, to indicate the presence of a particular DNA sequence thybridised on a transparent substrate in a three component sandwich assay format. Initially the capture oligonuclectide is immobilised onto a glass substrate. The target oligonuclectide is then hybridised to the capture oligonuclectide is then hybridised to the capture componential probes functionalised with target-complementary DNA. The signal can be enhanced, creating trees of nanoparticles, which can be consuming the chap especial sective and sensitive, but the re-use of the chips depended on the complete removal of the stain without damaging the chip. The advantage of these removal of the stain cre-cycled and re-used. The sequence presented is the capture of re-cycled and re-used. The sequence presented is the capture
                           귱
                  /note= "Forms a double-stranded region with bases 12-1
sequence ABS54437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid detection method; nanoparticle-oligonucleotide conjugate; nanoparticle; viral RNA detection; bacterial DNA detection; fungal DNA detection; nanoprobe conjugate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Removing silver from used DNA detection chips using cyanide etching solutions and ultrasound, allows chips to be re-cycled -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid detection method associated polynucleotide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                  /mod_base= "CTHER"
/note= "3' labelled with HS(CH2)3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8; DB 1;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 5; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACTCGTAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%;
                                                                                                                                                                                                                                                                                                                                       30-NOV-2001; 2001WO-US45039
                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000; 2000US-251715P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS64661 standard; DNA; 22
                                                                                                       /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOUN ) UNIV NORTHWESTERN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Park S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-698435/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                       WO200246483-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200246472-A2.
                                                                     modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mirkin CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS64661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS64661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is an oligonucleotide used in a method for detecting a nucleic acid having at least 2 portions. The method comprises hybridising the nucleic acid with holigonucleotides, such as the present sequence, attached to a substrate and/or particle and detecting a change in colour, conductivity or optical density. The method is useful for the diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing, for paternity testing, for cell line authentication and for monitoring gene therapy. Detecting nucleic acids based upon observing a colour change is cheap, fast, simple, and does not require specialised or expensive equipment. The nanoparticle oligonucleotide conjugates remain stable for at least 6 months. A single base mismatch and as little as 20 femtomoles (fM) of target can be detected using the conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics and DNA sequencing, comprises observing detectable change brought about by hybridization of nucleic acid with substrate or particle bound oligonucleotides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Silver staining; capture oligomucleotide; ss; DNA detection chip; gold nanoparticle; cyanide etching; ultrasound wave; sonication; pr three component sandwich assay; glass substrate; signal; detection; target-complementary DNA; tree; re-cycled; re-used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/bound_moiety= "Target oligonucleotide bases 12-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 1; Length 22;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silver staining method capture oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Fig 26; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACTCGTAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS54436 standard; DNA; 22 BP
                                                                                                                26-JUN-2000; 2000WO-US17507.
                                                                                                                                                                      25-JUN-1999; 99US-0344667
26-APR-2000; 2000US-0200161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                        MIRKIN C A.
LETSINGER R L.
MUCIC R C.
STORHOFF J J.
ELGHANIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-061976/07.
                                                                                                                                                                                                                                                                                                                                             (STOR/) STORHOFF J
(ELGH/) ELGHANIAN
(TATO/) TATON T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
WO200100876-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_binding
                                                   04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mirkin CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taton TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS54436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                         (LETS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABS54436
TD ABSS
XX
AC ABSS
XX
DT 28-N
XX
KW Silv
KW GOld
KW GOld
KW Thre
KW T
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Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change
                                                                                                                                         Mirkin CA, Letsinger RL, Mucic RC, S
Taton TA, Garimella V, Li Z, Park S;
                                                                                                                                                                                                                               Example 16; Page 151; 442pp; English.
                                                           11-DEC-2000; 2000US-255235P.
11-DEC-2000; 2000US-255236P.
12-JAN-2001; 2001US-0760500.
                        07-DEC-2001; 2001WO-US46418.
                                                                                    28-MAR-2001; 2001US-0820279
09-APR-2001; 2001US-282640P
                                          2000US-254392P
2000US-254418P
                                                                                                      10-AUG-2001; 2001US-0927777
                                                                                                                        (NANO-) NANOSPHERE INC.
                                                                                                                                                                   WPI; 2002-608256/65.
                                                  08-DEC-2000;
        13-JUN-2002
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The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligomolectides attached to it, which has a sequence complementary to sequence of two attached to it, which has a sequence complementary to sequence of two portions of mucleic acid, and nanoparticles, to allow hybridisation of oligomolectides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (M1), nanoparticles (I), nanoparticles (I), nanoparticles (I), nanoparticle (I), nanoparticles (I), nan Length 22; 1.4%; Score 15.8; DB 1; Length 2; 89.5%; Pred. No. 3.8e+02; ive 0; Mismatches 2; Indels Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other; 89.5%; Query Match

1076 CAACTATTAAAAAAAAA 1094 Local Similarity 89.5 es 17; Conservative **datches** à g

4 chacicginahahahaha 22

ABS64664 standard; DNA; 22 ABS64664; RESULT 645 ABS64664

BP

(first entry) 15-NOV-2002

Nucleic acid detection method associated polynucleotide #46.

Nucleic acid detection method; nanoparticle-oligonucleotide conjugate; nanoparticle; viral RNA detection; bacterial DNA detection; fungal DNA detection;

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Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change
                                                                                                                                                    Elghanian R;
                                                                                                                                                    Storhoff JJ,
                                                                                                                                                  RL, Mucic RC,
V, Li Z, Park
                                                                                                                                                                                                                              Example 17; Fig 26B; 442pp; English.
                                                                    2000US-254418P

2000US-255235P

2000US-255236P

2001US-0760500

2001US-0820279

2001US-282640P

2001US-09277777
                                             07-DEC-2001; 2001WO-US46418.
                                                                                                                                                 Mirkin CA, Letsinger RL
Taton TA, Garimella V,
                                                                                                                                  (NANO-) NANOSPHERE INC.
                                                                                                                                                                         WPI; 2002-608256/65.
               WO200246472-A2.
                                                                            11-DEC-2000;
11-DEC-2000;
12-JAN-2001;
                                                                                                   28-MAR-2001;
09-APR-2001;
                                                                                                                   10-AUG-2001;
                                                            08-DEC-2000;
                               13-JUN-2002
Synthetic.
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Storhoff JJ, Elghanian R;

the inversions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by conjugates (II) and observing a detectable change brought about by conjugates (II) and observing a detectable change brought about by conjugates (II) and observing a brobe are useful for detecting two or more nucleic acids (from a biological source) having at least two conjugates (II) and the aggregate probe are useful for detecting two or portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic (II) is useful for preparing a nucleic acid bound to an electrode surface. (II) is useful for preparing a nucleic acid bound to an electrode surface. (II) and (III) are useful for fabrication, and for separating as selected nucleic acid having two portions from other nucleic acide analyte) in a sample. This sequence represents a commendation of the aggregate probe are useful for detecting an analyte (especially commendation) and expresents and processing an analyte of the aggregate probe are useful for detecting an analyte (especially commendation) and expresents and expressing an analyte of the aggregate probe are useful for detecting an analyte (especially commendation) and expressing an analyte of the aggregate probe are useful for detecting an analyte (especially commendation) and expressing an analyte of the aggregate probe are useful for detecting an analyte (especially commendation) and expressing an analyte (especially commendation) and expressing an analyte (especially expressing an entire expressing an entire expressing an entire expressing an The invention describes a method of detecting (M1) a nucleic acid having polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention.

Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

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Gaps

0

0 Score 15.8; DB 1; Length 22; Pred. No. 3.8e+02; 0; Mismatches 2; Indels 1.4%; 17; Conservative Local Similarity Query Match Matches

. 0

Gaps

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BP. ABS64691 standard; DNA; 22 (first entry) 15-NOV-2002 ABS64691; 646 ABS64691
ID ABS6
XX
AC ABS6
XX
XX
DT 15-7
XX
XX
XX
XX
XX
XX RESULT

Nucleic acid detection method associated polynucleotide #73.

Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

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The invention describes a method of detecting (MI) a nucleic acid having two portions, involving providing nanoparticles having oligomucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to portions of nucleic acid, and nanoparticles, to allow hybridisation of oligomucleotides with two or more portions of hybridisation. (MI), nanoparticles (I), nanoparticles by the hybridisation (MI), nanoparticles (I), nanoparticles (I), nanoparticle-oligomucleotide conjugates (II) and the aggregate probe are useful for detecting two or portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid having two portions from other nucleic acids (I), (II) and conversable or detecting an analyte (especially natural mania) assertly for fabrication, and for separating a selected the aggregate probe are useful for detecting an analyte (especially natural mania).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R; Garimella V, Li Z, Park S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention
nanoparticle, viral RNA detection, bacterial DNA detection, fungal DNA detection; nanoprobe conjugate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.8; DB 1; Length 22;
Pred. No. 3.88+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a sample. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 26; Fig 52B; 442pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACTCGTAAAAAAAA 22
                                                                                                                                                                                                    08-DEC-2000; 2000US-254392P.
08-DEC-2000; 2000US-254418P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-0820279.
09-APR-2001; 2001US-28640P.
10-AUG-2001; 2001US-092777777
                                                                                                                                                                 07-DEC-2001; 2001WO-US46418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK65023 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                       (NANO-) NANOSPHERE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-608256/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                           WO200246472-A2.
                                                                                                                                13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                          Mirkin CA,
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Taton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK65023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK65023
TD ABK6
XX
AC ABK6
XX
DT 02-5
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at least 2 portions comprising: (a) providing another actual New, may have at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonucleotides (OGN), where OGN has a sequence complementary control to the sequence of NA; (b) contacting NA and NP under conditions of effective to allow hybridisation of OGN with NA; and (G) observing a detectable change brought about by hybridisation of OGN with NA.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

Detecting analytes such as nucleic acids and proteins are useful for the diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic assays. In particular assays using OGN-NP conjugates prepared using completes comprising a staroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitive than assays employing conjugates prepared using a state linker. The OGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates as probes to a DNA target to be PCR annulified can be carried through the 30 or 40 heating colling cycles of the PCR and are still able to detect the amplicons represent mannary and causing contamination. ABM65055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a method of detecting a nucleic acid (NA) having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridising nanoparticles with attached oligonucleotides to nucleic acid and detecting change brought about 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Storhoff JJ, Elghanian R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 15.8; DB 1; Length 22;
89.5%; Pred. No. 3.8e+02;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represent nanoparticle-oligonucleotides of the invention
                                     Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Mucic RC, SI
. Z, Park S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Page 407; 412pp; English.
 Nanoparticle-oligonucleotide #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                              Letsinger RL, Mucic
                                                                                                                                                                                                                                                               08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-0820279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CAACTCGTAAAAAAAA
                                                                                                                                                                                                        10-AUG-2001; 2001WO-US25237.
                                                                                                                                                                                                                                              2000US-224631P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK65026 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Garimella V,
                                                                                                                                                                                                                                                                                                                                                         (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-258024/30.
                                                                                                                                WO200218643-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisation
                                                                                                                                                                                                                                            11-AUG-2000;
                                                                                                                                                                     07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                              GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2002
                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 raton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK65026;
                                                                                                                                                                                                                                                                                                                                                                                          Mirkin
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ID ABK6
XX
AC ABK6
XX
DT 02-J
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02-JUL-2002 (first entry)

Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection; 88.

WO200218643-A2.

Synthetic.

07-MAR-2002

Nanoparticle-oligonucleotide #73

02-JUL-2002 (first entry)

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Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection; ss.
     Nanoparticle-oligonucleotide #46.
                                                                       11-AUG-2000; 2000US-224631P.
08-DEC-2000; 2000US-254932P.
11-DEC-2000; 2000US-25535E.
12-JAN-2001; 2001US-0766500.
28-MAR-2001; 2001US-0820279.
                                                             10-AUG-2001; 2001WO-US25237.
                                                                                                                 Letsinger RL,
Garímella V, I
                                                                                                      (NANO-) NANOSPHERE INC.
                                        WO200218643-A2.
                                                   07-MAR-2002
                                                                                                               Mirkin CA,
                               Synthetic
                                                                                                                      Taton TA,
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Storhoff JJ, Elghanian R;

RL, Mucic RC, St 7, Li Z, Park S;

Letsinger RI Garimella V,

G,

(NANO-) NANOSPHERE INC

Storhoff JJ, Elghanian R;

Mucic RC, S' Z, Park S;

ij

08-DEC-2000; 2000US-254332P. 11-DEC-2000; 2000US-255235P. 12-JAN-2001; 2001US-0760500. 28-WAR-2001; 2001US-0820279. 11-AUG-2000; 2000US-224631P. 10-AUG-2001; 2001WO-US25237.

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The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with at least 2 portions comprising: (a) providing nanoparticles (NP) with a traded oligonucleotides (OGN), where OGN has a sequence complementary content of NA; (b) contacting NA and NP under conditions of the sequence of NA; (b) contacting NA and NP under conditions of detectable change brought about by hybridisation of OGN with NA.

CC detectable change brought about by hybridisation of OGN with NA.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

CC diagnosis of genetic, bacterial and wiral diseases. The OGN-NP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic that use cyclic disulphide linkers improve the sensitivity of diagnostic linkers comprishing a steroid residue attached to a cyclic disulphide have semploying conjugates prepared using alkanethiols or acyclic disulphides of irrectly in PCR solutions. Therefore conjugates added as probes to a DNA cooling cycles of the PCR and are still able to detect the amplicas without opening the tubes and causing contamination. ABK65055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent nanoparticle-oligonucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
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                                    Gaps
                                    ,
  1.4%; Score 15.8; DB 1; Length 22; 89.5%; Pred. No. 3.8e+02; ive 0; Mismatches 2; Indels
               89.58;
                            17; Conservative
               Local Similarity
Query Match
                            Matches
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22 4 CAACTCGTAAAAAAAAA

g

ABK65053 RESULT 649 ABK65053 ID ABK6 XX AC ABK6

ABX92165;

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WPI; 2002-258024/30.
                                                                                                                               Taton TA,
                                                                                                                         Mirkin
                                                                                                                                                                                                                                                                                                                                                                       RESULT 650
                                                                                                                                                                                                                                                                                                                                                                             ABX92165
ð
                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                          Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridising nanoparticles with attached oligomucleotides to nucleic acid and detecting change brought about hybridisation.
                                                                                                                                                                     Example 17; Figure 26B; 412pp; English.
                                                                                                                                                                                                                                                                                                                                   1076 CAACTATTAAAAAAAAA 1094
                                                                                                                                                                                                                                                                                                                                                                        ABK65053 standard; DNA; 22
                                                                                                                                WPI; 2002-258024/30.
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the invention retailes to a method or detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonucleotides (OGN), where OGN has a sequence complementary concludes the sequence of NA; (b) contacting NA and NP under conditions of effective to allow hybridisation of OGN with NA; and (C) observing a detectable charge brought about by hybridisation of OGN with NA.

The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

C diagnosis of genetic, bacterial and viral diseases. The OGN-NF conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic that use cyclic disulphide linkers incomprising a steroid residue attached to a cyclic disulphide have sensitive than assays comportising a steroid residue attached to a cyclic disulphide have employing conjugates prepared using alkanethicles or acyclic disulphides of inkers comprising a steroid residue attached to a cyclic disulphides conjugates prepared using alkanethicles or acyclic disulphides as the linker. The OGN-NF conjugates are stable allowing them to be used directly in PCF solutions. The referee conjugates added as probes to a DNA carried through the 30 or 40 heating colling cycles of the PCR and are still able to detect the amplicons without popular or peaning or action or acti
                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a method of detecting a nucleic acid (NA) having
Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridising nanoparticles with attached oligonucleotides to nucleic acid and detecting change brought about 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No. 3.8e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent nanoparticle-oligonucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                  Example 28; Figure 52; 412pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076 CAACTATTAAAAAAAAA 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX92165 standard; DNA; 22 BP
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                                                                                                                                                                           hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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This invention describes a novel method of detecting nucleic acid having at least two portions. The method involves providing nanoparticles attached to oligomuclectides, where the oligomuclectide on each canoparticle have a sequence complementary to a sequence of at least two portions of nucleic acid, contacting nucleic acid and nanoparticle to callow hybridisation of the oligomuclectide on the nanoparticle to callow hybridisation of the oligomuclectide on the nanoparticle with two or more portions of nucleic acid and observing a detectable change or uncleic acid. The method is useful for separating a selected nucleic acid the aving at least two portions, from other nucleic acids and for acid having at least two portions. The method is useful for detecting any type of nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids. Preferably, the method is useful for detecting nucleic acids for diagnosis and/or monitoring of viral infections (human immundeficiency virus (HIV), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually transmitted diseases, inherited diseases, acuthentication, and for monitoring of the presencing, in the field to cresarch and analytical laboratories in DNA sequencing, in the field to non whenevirus and specialic pathogons. Detecting nucleic acids based on whenevirus and special pathogons. Detecting nucleic acids acids hased
                                                                                                        Nonoparticle, nucleic acid detection, hybridisation, diagnosis, sequencing, viral infection, human immunodeficiency virus, HIV; hepatitis virus, herpes virus, cycomegalovirus, Bpstein-Barr virus, bacterial infection, sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detect the presence of specific pathogens. Detecting nucleic acids base on observing a colour change with the naked eye is cheap, fast, simple and robust and does not require specialised expensive equipment. ABX92123-ABX92186 and ABQ77356 represent oligonucleotides used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting nucleic acids having at least two portions involves use of nanoparticles which have oligonuclectides attached to them that are complementary to portions of the nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R,
                                                                  Nanoparticle-associated oligonucleotide SEQ ID 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 16; Page 57; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   96US-031809P.
2000US-200161P.
2000US-0603830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US12783.
99US-0240755.
99US-0344667.
                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2001; 2001US-0967409
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NANO-) NANOSPHERE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-182627/18.
                                                                                                                                                                                                                                                                                      US2002155458-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2000;
                         12-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                 24-OCT-2002
                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taton TA;
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Gaps
                                                                              0;
                                    1.4%; Score 15.8; DB 1; Length 22; 89.5%; Pred. No. 3.8e+02; iive 0; Mismatches 2; Indels
Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                     17; Conservative
                                                      Best Local Similarity
                                  Query Match
                                                                   Matches
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4 CAACTCGTAAAAAAAAA 22

22

ABX92168 standard; DNA;

RESULT 651 ABX92168 (first entry)

12-MAY-2003

ABX92168;

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sequencing; viral infection; human immunodeficiency virus; HIV; hepatitis virus; herpes virus; cytomegalovirus; Bostein-Barr virus; bacterial infection; sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication; gene therapy; ss.
                                            Nonoparticle; nucleic acid detection; hybridisation; diagnosis;
                                Nanoparticle-associated oligonucleotide SEQ ID 46.
                                                                                                                                                2000US-200161P.
2000US-0603830.
97WO-US12783.
99US-0240755.
                                                                                                                            28-SEP-2001; 2001US-0967409
                                                                                                                                          96US-031809P.
                                                                                                  US2002155458-A1.
                                                                                                                                                       26-JUN-2000;
21-JUL-1997;
                                                                                                                                         29-JUL-1996;
                                                                                                                                                 6-APR-2000;
                                                                                                                                                                          25-JUN-1999;
                                                                                                                                                                    29-JAN-1999;
                                                                                                               24-OCT-2002.
                                                                                     Synthetic.
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(NANO-) NANOSPHERE INC.

Mucic RC, Storhoff JJ, Elghanian Letsinger RL, Mirkin CA, Taton TA;

Detecting nucleic acids having at least two portions involves use of nanoparticles which have oligonuclectides attached to them that are complementary to portions of the nucleic acid sequence WPI; 2003-182627/18.

Example 17; Figure 26; 130pp; English.

This invention describes a novel method of detecting nucleic acid having at least two portions. The method involves providing nanoparticles at least two portions. The method involves providing nanoparticles at least two can properticle to an apparence of at least two portions of mucleic acid, contacting nucleic acid and nanoparticle to allow hybridisation of the oligonucleotide on the nanoparticle with two cor more portions of mucleic acid and observing a detectable change brought about by hybridisation of the oligonucleotide nanoparticle with two correct two portions. The method is useful for separating a selected nucleic acid acids. The method is useful for separating a selected nucleic acid acids having at least two portions. The method is useful for detecting any type of mucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids. Preferably, the contioning of viral infections (numan immunodeficiency virus (HIV), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus), concerning diseases, sexually transmitted diseases, inherited disorders, in forensics, in DNA sequencing, for paternity testing, for cell line research and analyticial laboratories in DNA sequencing, in the field to authentication, and for monitoring gene therapy. The method is useful in cesearch and analyticial pathogens. Detecting nucleic acids based on observing a colour change with the naked eye is cheap, fast, simple conditional adoes not require specialised expensive equipment. illustrate the method of the invertion.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of detecting a nucleic acid using coligonucleotides (OG) attached to nanoparticles. The OG on each tamoparticle have a sequence complementary to the sequences of at least two portions of the nucleic acid being detected. Contacting between the hybridisation conditions, where binding is detected via a colour change. The method has applications in diagnosis of a diseases (e.g. diagnosing and monitoring viral diseases and as eystic fibrosis, cancers, etc.), in sequencing of authentication and for monitoring gene therapy. This sequence represents a DNA associated with the nucleic acid detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nanoparticles, where each oligonucleotide has a sequence complementary to at least two portions of the nucleic acid being detected, useful in diagnosis of a diseases (e.g. HIV)
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                              inherited disease; cystic fibrosis; cancer; sequencing; forensic; paternity testing; cell line authentication; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Storhoff JJ, Elghanian R;
                                                                 0;
                                                                                                                                                                                                                                                                                                                Nucleic acid detection; nanoparticle; HIV; bacterial disease;
                                                                                                                                                                                                                                                                                    Nucleic acid detection method associated oligonucleotide #42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a nucleic acid using oligonucleotides attached to
                                    Length 22;
                                                                Indels
                            Query Match
1.4%; Score 15.8; DB 1;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2;
Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mucic RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Column 60; 79pp; English.
                                                                                      1076 CAACTATTAAAAAAAA 1094
                                                                                                                     4 CAACTCGTAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-031809P.
99US-0344667.
97WO-US12783.
99US-0240755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0693005.
                                                                                                                                                                                            ABX98146 standard; DNA; 22
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mirkin CA, Letsinger RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-237646/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    US6495324-B1
                                                                                                                                                                                                                                                      16-MAY-2003
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21-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                          ABX98146;
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The invention describes a method of detecting a nucleic acid using objeonucleotides (OG) attached to nanoparticles. The OG on each nanoparticle have a sequence complementary to the sequences of at least two portions of the nucleic acid being detected. Contacting between the handparticle conjugated OG and nucleic acids takes place under hybridisation conditions, where binding is detected via a colour change. The method has applications in diagnosis of a diseases (e.g. diagnosing and monitoring viral diseases such as HIV, bacterial diseases, inherited nucleic acids, in forensics, for paternity testing, for cell line authentication and for monitoring gene therapy. This sequence represents a DNA associated with the nucleic acid detection method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementary
ted, useful in
                                                                                                                                                                                            Nucleic acid detection; nanoparticle; HIV; bacterial disease;
inherited disease; cystic fibrosis; cancer; sequencing;
forensic; paternity testing; cell line authentication; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a nucleic acid using oligonuclectides attached to nanoparticles, where each oligonuclectide has a sequence complementatio at least two portions of the nucleic acid being detected, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elghanian
                                                                                                                                                                 Nucleic acid detection method associated oligonucleotide #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 1; Length 22;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mucic RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 17; Fig 26B; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of a diseases (e.g. HIV)
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4 CAACTCGTAAAAAAAA 22
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99US-0344667.
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                                                                          ABX98149 standard; DNA; 22
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Letsinger RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-237646/23
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25-JUN-1999;
21-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
                                                                                                                                                                                                                                                                                                       US6495324-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999;
                                                                                                                                      16-MAY-2003
                                                                                                                                                                                                                                                                                                                                    17-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mirkin CA,
                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                      ABX98149;
                                            RESULT 653
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ABX79169 ID ABX79169 standard; DNA; 22 BP.

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Gaps

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2; Indels

Length 22;

1.4%; Score 15.8; DB 1; 89.5%; Pred. No. 3.8e+02;

0; Mismatches

0

Taton TA;

Nanoparticle, ss, nucleic acid detection, viral disease, probe, human immunodeficiency virus infection, hepatitis virus infection, detpes virus infection, cytomegalovirus infection, foremaic science, Epstein-Barr virus infection, bacterial disease; gene therapy, sexually transmitted disease, inherited disease; DNA sequencing, Immobilised capture probe for assay involving silver staining. paternity testing; cell line authentication 29-JUL-1996; 96US-031809P. 26-JRR-2000; 2000US-20016IP. 26-JUN-2000; 2000US-0603830. 21-JUL-1997; 97WO-USLZ783. 29-JAN-1999; 99US-0240755. 12-OCT-2001; 2001US-0976577. 99US-0344667. (first entry) (NANO-) NANOSPHERE INC. US2002155462-A1. 15-APR-2003 24-0CT-2002 25-JUN-1999; Synthetic ABX79169;

Storhoff JJ, Elghanian Mucic RC, Mirkin CA, Letsinger RL,

WPI; 2003-198491/19.

Detecting nucleic acids having at least 2 portions comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence -

Example 16; Page 37; 130pp; English.

The invention relates to detecting a nucleic acid (NA) having at least 2 portions, comprises providing a type of nanoparticles (NP) having attached to oligonuclectides (O) ((O) on each NP has a sequence of attached to oligonuclectides (O) ((O) on each NP has a sequence of an each NP has a detectable change brought about by hybridisation of (N) and observing a detectable change brought about by hybridisation of (O) on NP with NA. The nanoparticle is useful for separating a selected nucleic acid having at least 2 portions. The method of for detecting any type of nucleic acids and because of disease and in sequencing of nucleic acids for used for disgnosis of disease and in sequencing of nucleic acids for diagnosis and/or monitoring of viral diseases, for dispnosis and/or monitoring of viral diseases, inherited diseases, inherited diseases, in forenaics, in DNA sequencing for paternity testing, for virus, hepatitis virus, herpes virus, yetomegalovirus and Epstein-Barr (C disorders, in forenaics, in DNA sequencing, for paternity testing, for cell line authentication and for monitoring gene threapy. The method is cells for detect the presence of specific pathogens. Detecting and in each same and nobserving a colour change with the naked eye is cheap, the field to detect the presence of specific pathogens. Detecting and incoming and incoming and incoming and incoming and incoming and incoming based on observing a colour change with the naked eye is cheap, each simple and robust, and do not require specialised expensive particles) labelled probe used to demonstrate the method of the number on the colour change of the presence of the field the detect the presence of specialised expensive the number of the field the detect the number of the field to detect the presence of specialised expensive the number of the field to

/ Match
1.4%; Score 15.8; DB 1; Length 22;
Local Similarity 89.5%; Pred. No. 3.8e+02;
les 17; Conservative 0; Mismatches 2; Indels Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other; 17; Conservative Query Match Best Loca Matches

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Gaps

.; 0

2; Indels

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1076 CAACTATTAAAAAAAA 1094
                       4 CAACTCGTAAAAAAAA 22
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ABX79172 standard; DNA; 22

RESULT

15-APR-2003 (first entry) ABX79172;

CdSe/ZnS core/shell quantum dots oligonucleotide #1.

Nanoparticle, 88; nucleic acid detection; viral disease; probe; human immunodeficiency virus infection; hepatitis virus infection; herpes virus infection; cytomegalovirus infection; forensic science; Septein.Barr virus infection; bacterial disease; gene therapy; sexually transmitted disease; inherited disease; paternity testing; cell line authentication; quantum dot; semiconductor

Synthetic.

JS2002155462-A1.

24-0CT-2002

12-OCT-2001; 2001US-0976577.

29-JUL-1996; 96US-031809P. 26-APR-2000; 2000US-200161P. 26-JUN-2000; 2000US-0603830. 29-JUL-1996;

97WO-US12783. 99US-0344667 21-JUL-1997; 29-JAN-1999; 25-JUN-1999;

(NANO-) NANOSPHERE INC.

Storhoff JJ, Elghanian R; Mucic RC, Letsinger RL, Mirkin CA, Taton TA;

WPI; 2003-198491/19.

Detecting nucleic acids having at least 2 portions comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence.

Example 17; Fig 26; 130pp; English.

The invention relates to detecting a nucleic acid (NA) having at least 2 portions, comprises providing a type of nanoparticles (NP) having attached to oligonucleotides (O) (O) on each NP has a sequence of at least 2 portions of NA), contacting NA and observing a detectable change brought about by hybridisation of (N), on NP with 2 or more portions of NA, and observing a detectable change brought about by hybridisation of (N) on NP with NA. The nanoparticle is useful for separating a selected nucleic acid having at least 2 portions, the method of respecting nucleic acids having at least 2 portions. The method of using NP is useful for detecting any type of nucleic acids, and the method of using NP is useful for detecting any type of nucleic acids for used for diagnosis of disease and in sequencing of nucleic acids for preferably, the method is useful for detecting nucleic acids for diagnosis and/or monitoring of viral diseases (human immunodeficiency virus, bepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr CC virus, bacterial diseases, sexually transmitted diseases, inherited diseases, in forensics, in DNA sequencing, for cell line authentication and for monitoring gene therapy. The method is consecuted in research and analytical laboratories in DNA sequencing and in the field to detect the presence of specific pathogens. Detecting nucleic acids based on observing a colour require specialised expensive equipment. The present sequence is a nanoparticle (e.g. gold

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying nucleic acid encoding novel sex-linked-tissue-linked receptors, useful for isolating odorant binding proteins or pesticide alternatives, by analyzing sequences from a male- and female-specific nucleic acid library
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is that of an oligonucleotide used in a method
particles) labelled probe used to demonstrate the method of the invention. In this case the oligonucleotides are immobilised onto semiconductor nanoparticle quantum dots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled receptor; odourant; receptor; olfaction; array; microarray; anosmia; attractant; arometic; pesticide; PCR; primer;
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                      Query Match
1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                          Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide used in cDNA library array.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/mod_base= OTHER
/note= "5' polyl:
                                                                                                                                                                                                                                                                                                                                                                                                                    4 CAACTCGTAAAAAAAAA 22
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31-JAN-2002; 2002US-353392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002; 2002WO-US09559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV74140 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INSC-) INSCENT INC.
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XX AC ABV7.

XXX ABV7.

XXX ABV7.

XXX G-pr.

XXX G-pr.

XXX G-pr.

XXX B-r.

XXX B-r
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region present in every CDNA clone serves as the 5' priming site.

Denaturing and washing leave anchored CDNA in each well. The library is now arrayed and normalised. The method was used to identify and isolate clones encoding G-protein coupled receptors, especially odourant receptors, and active effectors involved in the olfactory pathway of invertebrates and vertebrates, e.g. odourant binding proteins, or other olfactory neuronal proteins. The identified receptors and proteins are useful for identifying compounds that reduce a target animal's sensitivity to odours, for manufacturing compounds or devices that mask odours, or trapping invertebrates with odourants. Semiochemicals (e.g. arometics or pheromone mimetics) can be developed with desirable effects on specific species for the development of pest monitoring systems or non-toxic, species-specific pesticide alternatives, for controlling insect feeding and breeding behaviour, detecting the presence of small air-borne molecules, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for analysis of an RNA sample which comprises amplifying cDNA with first and second differently labeled primers and analysis of the amplified labeled cDNA. The method is useful for analyzing differential gene expression, for identifying and/or characterizing pharmacological activities or for identifying target genes. The use of different primer combinations allow more cDNAs to be amplified. The method also provides a more detailed analysis than prior art methods. This sequence represents a primer used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of RNA samples, useful for detection of differential gene expression uses two differently labeled primers
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                                                                                                                                                                                                                                                                                                                                                        Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amplification; detection; gene expression; primer; ss.
                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 15.8; DB 1;
89.5%; Pred. No. 3.8e+02;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 10; 10pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                              1080 TATTAAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 TGTCAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA detecting primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-257789/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19840731-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ89372;
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ89372/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
        à
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Page 287

AAC69375 standard; DNA; 22

AAC69375;

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22 CTTTGTAGCACAAAAGCAGGTA 1
                                         RESULT 659
                                                        AAC69375
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o;

Gaps

.. 0

4; Indels

0; Mismatches

81.8%;

Local Similarity 81.8 es 18; Conservative

Matches

548 CTCTGTAGCCCAACAGCAGGGA 569

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Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning. A sample of 371 DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer analysis (using the "Primer" program available from E. Lander, MIT). The STSs and cosmids were mapped by in situ hybridisation, somatic cell hybrid analysis or both. Using this method, 370 STSs specific for human chromosome 11 were generated and most of them were regionally mapped. This procedure illustrates a novel method for sequencing complex genomes, designated "sequence sampled mapping method is useful for the completion of high density sequence-based maps, and ultimately, for the complete complete complete.
                                                                                                                                                                                                                                                       sequence sampled mapping; genomic analysis; complex genome mapping; cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing complex genomes, present as fragments in a cosmid library - by sequencing end-specific nucleotides of each clone then correlating with spatial relationship of cosmid, esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 15.6; DB 1; Length 22;
81.8%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                       Chromosome 11 (locus D11S1037) STS primer cSRL-2c7-tZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See AAQ82001-Q82706 for STS primers.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 66; 128pp; English.
1083 TAAAAAAAAAAAA 1098
                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US06810.
                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0078471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0117952,
                                                                                                            AAQ82104 standard; DNA; 22
                                                                                                                                                                                          (first entry)
                              16 каааааааааааа
                                                                                                                                                                             (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammalian chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-036508/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing of genomi
See AAO82001-082706
                                                                                                                                                                                                                                                                                                                                      WO9429486-A1
                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1993;
07-SEP-1993;
                                                                                                                                                                         25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1994.
                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                            AAQ82104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                               AAQ82104/
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The invention training to the number of G69120) which encoded it. ABCT is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly of intracellular cholesterol trafficking in monocytes and fibrohasts, being conversellular cholesterol trafficking in monocytes and fibrohasts, being involved in cholesterol trafficking in monocytes and fibrohasts, being closated on chronesome 991, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, rangier disease (TD) and familial HDL deficiency (FRA). These diseases of fatinguishable in that TD is an autosomal recessive disorder, while cholesterol') in the blood correlate with a high risk of cardiovascular disease, coronary reteronary artery disease, but also cerebrovascular disease, coronary restences is a protective effects against constructs and transpence cells and non-human animals comprising human ABCI nucleic cardiovascular disease compounds of gene therapy for the treatment or prevention of acide, and methods of gene therapy for the treatment or prevention also recompasses compounds which mimic ABCI extreming whether a patient has an encompassed risk for cardiovascular disease compounds which mimic ABCI activity, compounds which compounds increased risk for cardiovascular disease can parient has an encompassed risk for cardiovascular disease can be used to polymorphisms in the
                                                                                                                                                                                                  high density lipoprotein,
                                                                                                                                                                                           ATP-binding cassette; HDL deficiency disorder; high density lipoprotein Tangiar disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary attery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to the human ABC1 cholesterol transporter protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, Niemann-Pick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WBC1 polypeptide is useful for treating diseases associated with biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                              Human ABC1 BAC contig polymorphic site, SEQ ID NO:274
                                                                                                                                                                       Human ABC1 cholesterol transporter; chromosome 9g31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson AR, Pimstone SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Fig 11; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0124702.
99US-0138048.
99US-0139600.
99US-0151977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2000; 2000WO-IB00532.
                                                                                   29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-587528/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                WO200055318-A2.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayden MR,
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The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide. RIP60 is a zinc finger protein. The nucleic acid binding domain of the RIP60 polypeptide is used to construct a non-viral nucleic acid delivery complex comprising a modular non-viral nucleic acid delivery complex comprising a modular poptide. The complex comprises a modular peptide containing a nucleic acid binding domain and a nucleic acid condensation domain and a nucleic acid condensation domain condenses in length. The complex also comprises one or more solvipoptides selected from a cell recognition domain, a protein transduction domain, a protein interaction domain, an intracellular transduction domain, a protein interaction domain, an epitope domain and a protein purification domain. The complexes are used to deliver a nucleic acid to a cell. The nucleic acids delivered are of various sizes and preferably greater than 50 kilobases, especially more than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-viral nucleic acid delivery complex for delivering a nucleic acid molecule into a cell comprises a modular polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence which is bound by 22 domain of RIP60 polypeptide.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; RIP60; zinc finger protein; nucleic acid delivery complex;
nucleic acid binding domain; nucleic acid condensation domain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is bound by the Z2 domain of the human RIP60
                                                                                                                                                                                        ;
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                                                                                                                                              1.4%; Score 15.6; DB 1; Length 22; 81.8%; Pred. No. 4.1e+02; ive 0; Mismatches 4; Indels
                                                                                                       Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                  991 TIGGAAGICTGAGGCTGGAGAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page 74; 115pp; English.
                                                                                                                                                                                                                                                   1 Tregenegernangecagenan 22
                                                                                                                                                                                                                                                                                                                                              BP
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99US-0114745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JAN-2000; 2000WO-US00212.
                                                                                                                                                                                                                                                                                                                                        AAA57767 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                      Query Match
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houchens CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-465985/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200040723-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heintz NH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           AAA57767;
                                                                                                                                                                                                                                                                                                       RESULT 660
                                                                           gene.
                                                                                                                                                                                                                                                                                                                      AAA57767,
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The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1 allelic variant polynucleotide. The polypeptides of the invention have neuroleptic activity. The polynucleotides may have a use in gene therapy. DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or Lreating a subject having a disease or disorder associated with specific DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g. neuropsychiatric disorder such as schizoaffective, bipolar, unipolar affective or adolescent conduct disorder or schizophrenia. Similarly, affective or adolescent conduct disorder or schizophrenia. Similarly, method for treating such neuropsychiatric disorders. The sequences shown in ABQ93575-ABQ93658 represent the PCR primers used in the invention to amplify the sequences of DISC2 and DISC2.
                                                                                                                                                                                                                                        Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy; neuropsychiatric disorder; schizoaffective disorder; bipolar disorder; unipolar affective disorder; adolescent conduct disorder; schizophrenia; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes containing single nucleotide polymorphisms, useful for preventing or treating neuropsychiatric disorders e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 4.1e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barnes GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parker A,
                                                                                                                                                                                                        Human DISC1/DISC2 PCR primer disc25 f2.
 1078 ACTATTAAAAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030 GCCIGGCITICATAGIGAGGCI 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Figure 4; 169pp; English.
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                              ACTAATAATAATAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrington-martin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GCCTAGACTTCACAGTGAGGCT
                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-2002; 2002WO-US02186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2001; 2001US-0770107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENIUM PHARM INC.
                                                                                                               ABQ93623 Standard; DNA; 22
                                                                                                                                                                            16-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590791/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                        WO200258637-A2.
                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyer JM,
                                                                                                                                             ABQ93623;
                                22
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                                                                               RESULT 661
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AAD31453
                                                                                              ABQ93623,
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Gaps

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Length 22; 4; Indels

Score 15.6; DB 1; Pred. No. 4.1e+02; 0; Mismatches 4;

Query Match 1.4%; Best Local Similarity 81.8%; Matches 18; Conservative

Sequence 22 BP; 5 A; 0 C; 1 G; 16 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods for distinguishing between individuals homozygous for and therefore afflicted with Van Buchem's disease, individuals heterozygous for and therefore carriers of Van Buchem's disease comprise identifying a large genomic deletion in chromosome 17 at 17q21. The method is useful for identifying individuals who are afflicted with or carriers of diseases associated with one or more genomic deletion, particularly Van Buchem's disease, which is a rare autosomal recessive disorder that results in a bone dysplasia referred to a craniotubular hypertosis. The present sequence is a PCR primer used to amplify 92Kb gene fragment in human chromosome 17 at 17q21.
                                                                                                              Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
autosomal recessive disorder; chromosome 17; chromosome 17q21;
bone dysplasia; 92Kb gene fragment; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, Van Buchem's disease; genomic deletion; craniotubular hypertosis;
autosomal recessive disorder; chromosome 17; chromosome 17421;
bone dysplasia; 92Kb gene fragment; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methods for identifying subjects who are afflicted with or carriers of diseases associated with genomic deletion(s), e.g. Van Buchem's disease, by determining the presence of a deletion in the 92 kb region of human chromosome 17 at 17q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                       Human chromosome 17 92Kb gene fragment amplifying PCR primer, WtlR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chromosome 17 92Kb gene fragment amplifying PCR primer, Wt3R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.6; DB 1;
Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 26; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paeper B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tegendecreacecandada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELLTECH R & D INC.
STRAEHLING HAMPTON K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-221855P.
2001US-303386P.
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2001; 2001WO-US23968
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proll S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-227089/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           WO200210455-A2
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                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
   31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunkow ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                         07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STRA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 663
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NAMES OF COLOR OF STREET O
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The present invention relates to methods for distinguishing between individuals homozygous for and therefore afflicted with Van Buchem's disease, individuals hererozygous for and therefore carriers of Van Buchem's disease and individuals who are not afflicted with Van Buchems's disease comprise identifying a large genemic deletion in chromosome 17 at 17q21. The method is useful for identifying individuals who are afflicted with or carriers of diseases associated with one or more genomic deletion, particularly Van Buchem's disease, which is a rare autosomal recessive disorder that results in a bone dysplasia referred to a cranicubular hypertosis. The present sequence is a PCR primer used to amplify 92Kb gene fragment in human chromosome 17 at 17q21.
                                                                                                                                                                                                                                 Methods for identifying subjects who are afflicted with or carriers of diseases associated with genomic deletion(s), e.g. Van Buchem's disease, by determining the presence of a deletion in the 92 kb region of human chromosome 17 at 17q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonuclectide; gene expression modification; cancer; phosphorothicate; endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 15.6; DB 1; Length 2:
31.8%; Pred. No. 4.18+02;
Ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992 TGGAAGTCTGAGGCTGGAGAAT 1013
                                                                                                                                                                                                                                                                                                             Example 3; Page 26; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGAGGCTGAGGCAAGAGT 22
                                                                                                                                                                           ä
                                                                                                                                                                         Paeper
                                                                                                                        CELLTECH R & D INC.
STRAEHLING HAMPTON K.
                                            30-JUL-2001; 2001WO-US23968.
                                                                              28-JUL-2000; 2000US-221855P.
06-JUL-2001; 2001US-303386P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
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98US-0103636.
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ID AAA25452 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                      Proll S,
                                                                                                                                                                                                     WPI; 2002-227089/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                           28-JUL-2000;
                                                                                                                                                                        Brunkow ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1999;
              07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09954459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1998;
23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                       (STRA/)
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to transforming cells ex vivo and implanting transforming cells ex vivo and implanting conference conditions associated with levels of the conference conditions associated with levels of alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of and/ifications in (A) improves resistance to nucleases, binding affinity and/ifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24748 to AAA25992 represent their corresponding target sequences, and AAA25107 to AAA2519 represent cheir orresponding target sequences. AAAA5519 to AAA26107 represent their receptor hairpin ribozyme sequences. AAAA5519 to AAA2617 represent their corresponding target sequences. AAAA56107 to AAA2618 represent their corresponding target sequences. AAAA56107 to AAA2617 represent their corresponding target sequences. AAAA2619 to AAA26271 represent their corresponding target sequences. AAAA2619 to AAA2617 represent their corresponding target sequences. AAAA26107 to AAA2617 represent their corresponding target sequences. AAA26191 to AAA2617 represent their corresponding target sequences. AAA26107 to AAA2617 represent their exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
           Bellon L;
                                                                                                                                                                                                        nucleic acids that interact, and optionally cleave, target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
           Karpeisky A,
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;
n L, McSwiggen JA,
Jarvis T, Woolf T,
                                                                                                                                                                                                                                                                                                                Claim 77; Page 79; 148pp; English.
                                                                                                                                                                                                                                                 sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA25453 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ACAAAAAAAAAAAAA 1
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   Beigelman L,
Zwick M, Jar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                         WPI; 2000-013248/01
                                                                          Matulic-Adamic J;
   Thompson JD,
Reynolds M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2000
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23-JUN-1998;
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AC AAA2
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KW DAMM
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Bellon L;

Beigelman L, McSwiggen JA, Karpeisky A, Zwick M, Jarvis T, Woolf T, Haeberli P;

Thompson JD, Reynolds M,

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with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or conductions associated with levels of casted cells, or for other conditions associated with levels of can also be used to correlate inhightion of gene expression with contractions in phenotype, particularly for identification of therapeutic targets, and as research reagents (for NA, in the same way that restriction endonucleases are used with DNA). The combination of and/or activity. AAA23503 to AAA24748 to AAA25992 represent their corresponding target sequences, and AAA25107 to AAA25192 represent their corresponding target sequences, and AAA25107 to AAA2518 represent centrogen receptor alripin ribozyme sequences. AAA25993 to AAA26107 to AAA2511 represent their corresponding target sequences. AAA25991 to AAA2611 represent their corresponding target sequences. AAA25991 to AAA2611 represent centrogen receptor alripin ribozyme sequences. AAA25991 to AAA2611 represent corresponding target sequences. AAA25991 to AAA2611 represent centrogen corpus ribozyme sequences. AAA25991 to AAA26211 represent corpus corpus and antisense oligonucleotides used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                          present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequential consensus region-directed amplification for sorting mixture of DNAs into 2 or more subsets or distinguishing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo-AT PCR primer #2 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequential consensus region-directed amplification, gene expression, disease diagnosis; gene analysis; human; matrix metalloproteinase;
                                                                             New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; Score 15.4; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillies G;
                                                                                                                                 Claim 77; Page 79; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083 TAAAAAAAAAAAA 1099
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Best Local Similarity 94.1
Matches 16; Conservative
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                                      WPI; 2000-013248/01.
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Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6277571-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD44151;
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The invention relates to a method of segmential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo AT PCR primer used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probes for detecting target nucleotide sequence in sample, has sequence that forms hairpin structure having a double-stranded segment and single-stranded loop collectively forming region complementary to
 in 2 samples, useful for disease diagnosis and gene analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide AGT02014. This is one of a set of oligonucleotides (see ABBA91527-30) used to assess the minimum number of ribonucleotides in DNA-RNA chimeric oligonucleotides required for RNase H cleavage. Each oligonucleotide of the set had a different number of ribonucleotides, in the present case. The oligonucleotides were mixed with target DNA oligonucleotide AGT02009 (see ABA91531) and incubated with RNase H (5 U/Ml) at 37 degrees C for 30 minutes. The results showed that 4 ribonucleotides were the minimum number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
                                                                                                                                                                                                                                    Query Match 1.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
                                                                                                                                                                                                    Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;
                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                socation/Qualifiers
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                                                                                                                                                                                                                                                                                                       1084 AAAAAAAAAAAAAA 1100
                                 Example; Fig 1D; 19pp; English.
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/label= "RNA"
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30-MAR-2001; 2001US-0823647
                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAABA
                                                                                                                                                                                                                                                                                                                                                                                                                          ABA91530 standard; DNA; 17
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                                                                                                                                                                                                                                                                     16; Conservative
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misc_RNA
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for RNA cleavage. The invention provides probes for nucleic acid hybridisation. The probes form a hairpin structure comprising a double-stranded stem and a single-stranded loop, and are capable of both intramolecular and intermolecular hybridisation. The double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that is resistent to RNAse H Gleavage. When the probe hybridises with a target DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and can be removed. Arrays and methods for nucleic acid hybridisation using the probes are provided.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       deoxyribonucleic acid; major groove; ethanoamino group; tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The oligomer was designed to target human TNF receptor mRNA beginning at nucleotide 2354 and to covalently cross-link to the target via the N4N4-ethanocytosine group. See also AAQ20109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New sequence-specific non-photo-activated crosslinking agents -
bind to the major groove of duplex DNA and are esp. useful for
treating latent infections e.g. HIV
                                                                                                                                                                                                                                                                                                                                                                                                             Cross-linking oligomer 942 to target human INF Receptor mRNA.
                                                                                                                                                                          Length 17;
                                                                                                                                                                                                     Indels
                                                                                                                                                                      1.4%; Score 15.4; DB 1;
94.1%; Pred. No. 3.4e+02;
Ve 0; Mismatches 1;
                                                                                                                                         Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 other;
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-linking group; ss.
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modified_base
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AAQ25501 standard; DNA; 18
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17-APR-1991;
17-APR-1991;
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                                       25-MAR-2003
07-DEC-1992
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18-JAN-1991;
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                       AAQ25501;
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                      Gaps
                                                                                                                                                                   deoxyribonucleic acid; major groove; ethanoamino group;
tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
cross-linking group; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The oligomer was designed to target human TNF receptor mRNA beginning at nucleotide 2354 and to covalently cross-link to the target via the N4N4-ethanocytosine group. See also AAQ20108.
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bind to the major groove of duplex DNA and are esp. useful for
treating latent infections e.g. HIV
                                                                                                                                                 Cross-linking oligomer 943 to target human INF Receptor mRNA.
Query Match
1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "N4N4-ethanocytosine"
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 27; 42pp; English.
                                                                                                                                                                                                                                          *tag= a
'mod_base= OTHER
                                   1084 AAAAAAAAAAAAA 1100
                                                                                                 BP.
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90US-0529346.
                                                                                                                                                                                                                                                                                                                                                 91WO-1003680
                                                                                               AAQ20109 standard; DNA; 18
                                                                                                                                 01-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Krawczyk S;
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modified_base
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                                                                                                                                                                                                                                                                modified base
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25-MAY-1990;
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                                                                                                                 AAQ20109;
                                                                            RESULT 669
                                                                                       AAQ20109/
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The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA sequence obeginning at nucleotide 2354. The sequence is a viral duplex sequence contg. a purime-rich region concentrated on one chain of the duplex. The sequence may be prepd. by standard DNA synthesis. The tumner are dapable of forming a triplex at physiological pH by coupling into are capable of forming a triplex at physiological pH by coupling into the major groove of the DNA duplex. Three such oligomers WIRP 941-22 are capable of forming a triplex with this sequence. The oligomers may be used to target viral DNA duplexes specific for HIV, herpes and cher viruses. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer is able to inhibit gene expression, see also AAQ25452-25500 and AAQ30226-448.
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                                                                                                                              Target; human tumour necrosis factor receptor mRNA; AIDS; triplex;
HIV; hepatitis; malignancy; inflammation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
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                                                                        Purine rich HUMNFR target duplex sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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91US-0643382.
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January 8, 2004, 16:08:28; Search time 35 Seconds (without alignments) 1.937 Million cell updates/sec

score: Sequence: Title: Perfect :

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

1682 seqs, 30821 residues Searched:

3364 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 12 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1690 summaries

rng1.seq:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Reverse transcript	Human medsin promo		rse trans				Anchored poly T RT	genome	transcri									c			Jymorphic	•==	transcri	transcri	transcri	transcri	transcri	transcri		transcri	transcri	
SUMMARIES	ID		AAQ/5/28	AAA71444	AAH38447	AAQ75581	AAQ75727	AAQ75729	AAQ75730	AAV71936	ABK52620	AAQ75724	AAQ75732	AAQ75760	AAQ75696	AAQ75712	AAQ75720	AAQ75680	AAQ75675	AAQ75632	ABK12409	AAI66361	ABK86170	ABX79828	AAQ75552	AAQ75580	AAQ75582	AAQ75579	AAQ75723	AAQ75725	AAQ75726	AAQ75731	AAQ75733	AAQ75734	AAQ75719
	DB	-	4	Н	Н	Н	Н	Н	Н	Н	П	-1	Н	Н	Н	٦	Н	~	٦	н	н	۲-4	٦	 1	Н	Н	П	Н	Н	~1	Н	н	Н	Н	Н
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Reverse transcript Reverse transcript Oligo dT primer #1 Oligo dT primer #2 Anchored poly T RT Human gene specifi Human Grophilin- PCR primer for hum 16s rRNA gene PCR Human pancraatic P Human B8124 specif Reverse transcript	te transcripe e transcripp e tr	
AAQ75721 AAQ75722 ABK86168 ABK86169 AAV1035 AAL47515 AAX44258 AAX96240 AAX78723 AAX78723 AAX78723	AAQ75589 AAQ75587 AAQ75587 AAQ75587 AAQ75575 AAQ75592 AAQ75592 AAQ75693 AAQ75633	AAQ75578 AAV07752 AAV13753 AAS10448 AAS104112 AAS04213 AAS04213 AAS04213 AAC75691 AAQ75693 AAQ75693 AAQ75693 AAQ75693
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AAA91207 AAQ75751 AAQ75753 AAQ75753

HLA HLA-C gene PCR Rapid capture prob Capture probe CP12 Example oligonucle Reverse transcript ...use total gene-Spearmint (-)-limo HOOK PCK primer us Rabbit atheroscler CNS related 3' seq Reverse transcript Reverse transcript Reverse transcript Human polymorphic Human polymorphic Reverse transcript
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3'-PCR primer used transcript transcript pr DNA topoisomerase Leukaemia related Human actin simila Aspergillus niger Human alkylation D RT-PCR primer of t transcript transcript PCR primer. Synth Anchored poly(T) o Anchored poly(T) o Nucleotide sequenc transcript transcript plas transcript transcript (-)-limonene-6-hyd Primer HOOK for cD 3' sequencing prim Mouse microglia an Mouse total gene e transcript n receptor of a micr Human retrovirus H 2'-Methoxyethoxy-m Human protein AQ2 Nuclease resistant Primer SEQ ID NO:2 transcrit transcrit transcri transcri transcri Phosphorothioate fragment of a p Template mRNA p RT-PCR primer o Antisense I Reverse tra Reverse tra Oestrogen Reverse Revers Sequence

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                                                                                                                                     A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESED files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
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                                                                                           of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA for promoter region of megsin useful for screening proteins
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Best Local Similarity
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(MIYA/) MIYATA T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Wyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatooid arthritis; multiple solerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
for screening and isolating proteins (especially transcription AAA71434-A71469 represent PCR primers used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - AAH40944 represent PCR primers, single nucleotide
                                                                                                                                                                                                                                                                                                                                                                           ٠.
                                                                                                                                                                                                                                                                 1.9%; Score 21; DB 1; Length 30; 82.8%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                   T; 0 other
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       266 GAGCACCTTCAGAAGTTGTTGAAACTTG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCAGCTTCAGATAGGAGCTGAAACTTG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNPE primer SEQ ID 1243.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                            Sequence 30 BP; 6 A; 10 C; 5
                                    factors). AAA71434-A71469 redescribed in the invention.
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Best Local Similarity
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Matches

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AAQ75581,

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and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers
                                                                                                                                      gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 66; Cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 11pp; Japanese.
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                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-018287/03.
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Best Local Similarity
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                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                       16-APR-1993;
                                                              04-AUG-1995
                                                                                                                                                                                                                                                                                                                         16-APR-1993;
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                                                                                                                                                        aggregate;
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                                AAQ75727;
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inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ752781) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                             Length 25;
                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 63;
ive 0; Mismatches 0; Indels
                                                                                                                                           DB 1;
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                                                                                                      BP; 6 A; 2 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                        Score 20.2; I
Pred. No. 74;
                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggregate; restriction enzyme; ss
                                                                                                                                                                                                                                                                                                                               BP.
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AAQ75727/c
ID AAQ75727 standard; DNA; 21 BP.
                                                                                                                                        1.8%;
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AAQ75581 standard; DNA; 20
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                                                                                                                                                    Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analysis; gene
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                                                                                                      Sequence 25
                                                                                                                                                                    22;
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                                                                     sequence.
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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             Analysis of followed by
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followed by
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aggregate;
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                                                                      Query Match
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Matches
                                                                                                      AAQ75730/c
                                                                                                   RESULT 7
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The invention relates to preparation of a normalised, subdivided library of amplified cDNA from the coding regions of mRNA in a sample. The method livolves transfers transfersibility, with at least one CDNA primer of formula 5'-Conl-dTn2-Vn3-Nn4 to form first stand cDNA where Conl = any sequence of 1-100 nucleotides; dT = deoxythymidinyl; nZ is at least 1, n3 and and are both 0, or n3 is 1 and n4 is at least 1; followed by second strand cDNA synthesis using the first strand as template and a second cDNA primer of a similar formula, in the presence of DNA polymerase I (or strand cDNA primer of a similar formula, in the presence of DNA polymerase I (or famplification primers. Comparison of cDNA in the prepared library with a database (a computer-generated list of molecular weights of restricted DNA fragments of known sequence) is used to determine presence of an adatabase (a computer-generated list of molecular weights of restricted DNA fragments of known sequence) is used to determine presence of an computed adaignosis of disease). Surfaces (ching) having maplified cDNA stably immobilised on it, obtained by a similar method, with nucleic acid from the family (to identify new genes) and to detect differences in expression patterns between cells. The polypeptides C expressed by the libraries can be used for drug development. Sequences ANV1935 to ANV1946 represent primers used to exemplify the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of normalised, subdivided cDNA libraries from mRNA - by reverse transcription and amplification, used to screen for new genes and interacting proteins, potential drugs, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                               Normalised, cDNA library; mRNA cloning; reverse transcription; immobilise; screening; hybridisation; nucleic acid amplification; expression pattern; drug development; PCR primer; RT-PCR; ss.
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                                                                Mismatches
                Score 20;
Pred. No.
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1.8%; Sc.
100.0%; Pre
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                                                                                                                                                       ATTAAAAAAAAAAAAAAA
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97DK-0000547.
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                                      Similarity
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19-MAY-1997;
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              Query Match
Best Local &
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                                                                                                                                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESED files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       amplification of mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                     CDNA and gene expression - by ampl digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 20; DB 1;
.00.0%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 66;
live 0; Mismatches
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                                                                                                                               Disclosure; Page 8; 11pp; Japanese.
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                                                                   CDNA and
                     WPI; 1995-018287/03.
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les 20; Conserv
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Length 27;

1.8%; Score 19.6; DB 1;

Query Match

Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;

Thu Jan

RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new method for detecting minority genomes, present at less than 50%, in a population of nucleic acids of a viral quasi-species and having at least one mutation with respect to the majority genome. The invention can be used for genetic diagnosis of viral infections, especially human immune deficiency virus and heptitics B or C, particularly to detect memory minority genomes that are implicated in failure of antivixal therapy, so the method may make possible design of therapies customised for individual patients. The present nucleic acid sequence represents the VRA-MOT-11 DNA sequence that was used in the methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baranowski E, Briones Llorente C, Domingo Solans E; Gomez Castilla J, Martin Ruiz-jarabo C;
                           Gaps
                                                                                                                                                                                                                                                                             Minority genome method; viral quasi-species; majority genome; genetic diagnosis; viral infection; human immune deficiency virus; hepatitis B; hepatitis C; antiviral therapy; ss.
                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting minority genomes in viral quasi-species, useful for identifying mutants responsible for drug resistance and to individualise therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 19.6; DB 1; Length 27; 84.6%; Pred. No. 1e+02; ative 0; Mismatches 4; Indels
                      Indels
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|label= unknown
|note= "C6 aminolinker sequence"
                                                                                                                                                                                                                                              Minority genome method VFA-MUT-11 DNA sequence.
      Pred. No. 1e+02;
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84.6%; Prea. .v..
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                                                                                                                                                          BP.
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                                                                                                                                                       ABK52620 standard; DNA; 27
                                                                                                                                                                                                                    (first entry)
                   Conservative
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   Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
Matches 22; Conserv
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Escarmis Homs C,
                                                                                                                                                                                                                                                                                                                                                                       Key
misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parro Garcia V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200183815-A1.
                                                                                                                                                                                                                   27-AUG-2002
                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                          RESULT
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispsting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                        gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                               by amplification of mRNA enzymes
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                                                                            Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reverse transcription primer used in cDNA analysis technique.
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95.2%; Pred. No. 85;
live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression - followed by digestion with restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080 TATTAAAAAAAAAAAA 1100
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AAQ75724 standard; DNA; 21 BP.
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                                                     entry)
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                                                    (first
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                                                                                                                                                                    JP06303997-A.
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                                                                                                                                                                                              01-NOV-1994.
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                                                                                                                    aggregate;
                                                                                                                                             Synthetic.
                                                                                                     Analysis;
                           AAQ75724;
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1073 AAGCAACTATTAAAAAAAAAAAA 1098 ACGCGAGGATTAAAAAAAAAAAA 2

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Conservative

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Gaps

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
    seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; reverse transcription; primer; cDNA;
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                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
                                                                                                                                        Indels
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                                                                                                DB 1;
                                                          Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
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                                                                                                Score 19.4;
Pred. No. 85;
                                                                                                                                      0; Mismatches
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                                                                                                                                                                        1080 TATTAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggregate; restriction enzyme; ss.
                                                                                                                                                                                                              21 TATGAAAAAAAAAAAA 1
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                                                                                                  1.8%;
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AAQ75696 standard; DNA;
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                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
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                        rapidly and easily.
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                                                                                                                                                                                                                                                                                                                                                AAQ75696;
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AAQ75712/c
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AAQ75696/
    SXXS
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                                                                                                                                                                                                                                          A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 19.4; D
95.2%; Pred. No. 85;
ative 0; Mismatches
                                                                    (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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93JP-0112515.
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Pest Local Similarity 95.2.
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16-APR-1993;
                                  16-APR-1993;
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followed by
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of
                                                                                                                                                                                                          Disclosure;
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(first entry)

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                                                                                                             Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                   Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA and gene expression - by ampl digestion with restriction enzymes
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Pred. No. 85;
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                                                                                                                                       aggregate; restriction enzyme, ss
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AAQ75720 standard; DNA; 21
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                   Gaps
             of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                  Length 21;
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                                                                                                                                                                                                                                                                                  1.8%; Score 19.4; DB 1; 95.2%; Pred. No. 85;
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Pred. No. 85;
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                                                           Disclosure; Page 8; 11pp; Japanese
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AAQ75680 standard; DNA; 21
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                                                                                                                                                             lene expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                    cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
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95.2%; Pred. No. 85;
ive 0; Mismatches
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The present invention provides the protein and coding sequences of human phosphatichidylinosation. (PIDINS-3) Kinase 35. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, development discorders, immunological diseases and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and treating malignant tumor, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer; athy; development disorder; HIV infection; immunological disease;
          The present invention relates to the isolation of polypeptide-laminin B210.67, and the polypucleotide encoding it. Also described is the process for preparing the protein by DNA recombination. The polypeptide is useful for treating diseases such as embryo development teratogenesis. The present sequence for reverse transcriptase (RP)-PCR primer #1 is used with RT-PCR primer #1 is used with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-laminin B210.67.
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                                                                                                                                                                                     1.8%; Score 19.4; DB 1; Length 24; 95.2%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding sequence of the invention.
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;
                                                                                                                                                    Seguence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                          1080 TATTAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 12; 34pp; Chinese.
                                                                                                                                                                                                                                                                                           TCTTAAAAAAAAAAAAAA 23
                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2000; 2000CN-0114973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001WO-CN00328.
                                                                                                                                                                                                                                                                                                                                                                                 AAI66361 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-025836/03.
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175014-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  AAI66361;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
18
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                 AAI66361/
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The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having a specific oligo-dT primer sequence, where the identimer comprises a a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that are expressed at different levels between 2 or more samples, where that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene cypression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is continuation in addition to information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information concerning changes or differences in mRNA level, to determine mRNA expression level and mRNA identification in one assay; (c) generates cDNA fragments from all mRNAs present in the genome of the organism under investigation by common molecular biology corganisms lacking significant genomic sequence in formation. The present convertion in the method of the present invention in the method of the present invention in the method of the present invention in the method of the invention in the income represents an oligo of primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                             Oligo dT primer #3 used in method to study gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                     Oligo dT primer; gene expression analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.2; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dombkowski AA, Nagel AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 21; 45pp; English.
                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOMIC SOLUTIONS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.7%;
1 Similarity 87.5%;
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2000; 2000US-244933P.
                 ABK86170 standard; DNA; 25
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                                                                                                  24-SEP-2002
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                                                                                                                                                                                                                                Synthetic.
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Best Local S
                                                            ABK86170;
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ABK86170/
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Pred. No. 98; 0; Mismatches

ilarity 95.2%; Conservative

Query Match Best Local Similarity Matches 20; Conserv

1080 TATTAAAAAAAAAAAA 1100

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Score 19.4; DB 1; Length 24;

1.8%;

RESULT 22 ABX79828/c

17-APR-2003

ABX79828,

29-OCT-2002

Garner HR,

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A method for the analysis of cDNA comprises (a) preparing an aggregate of Gouble-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) (iles AAQ75547-Q7759) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                         cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                  Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reverse transcription primer used in cDNA analysis technique.
Reverse transcription primer used in cDNA analysis technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7%; Score 19; DB 1;
.00.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 other;
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                                                                                                                                                                                                                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 5; 11pp; Japanese
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by
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                                                                                                                                                                                                                                                                                                                                                                                           Analysis
followed
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AAQ75580/c
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat within a coding sequence (expressed sequence tay, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to mucleotide repeats are Machado-Joseph, Haw River
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX7676-ABX80022 are the polymorphic repeats identified for a search of human ESTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses a method for identifying a candidate polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                              EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POWPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Hutlington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.2; DB 1;
Pred. No. 1.2e+02;
                                                                                                                        repeat polynucleotide #153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fondon JW;
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      BP.
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1 Similarity 87.5%;
21; Conservative
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      ABX79828 standard; cDNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0475947
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                                                                                                                            EST polymorphic DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Best Loca Matches

AAQ75552;

AXXXEX XAXXXA

AAQ75552/c RESULT 23

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Length 19; Indels

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                                                             A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQV5547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 20;
Pred. No. 95;
                                                                                                                                                                                                                                                                                                     0; Indels
digestion with restriction enzymes
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                                                                                                                                                                                                                                                                     Query Match 1.7%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 95; Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5; 11pp; Japanese.
                                   Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction enzyme; ss.
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Best Local Similarity
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 followed
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (CBRESEQ files AAQ7554-0.05798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction serzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression rapidly and easily.
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Pred. No.
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Best Local Similarity 100.
Matches 19; Conservative
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AAQ75579/c
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restriction enzyme; ss.
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1e+02;
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Pred. No. 1e+02;
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AAQ75731/c
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AAQ75726/c
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AAQ75725 standard; DNA; 21
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followed by
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AAQ75731 standard; DNA; 21

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75747-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                          aggregate; restriction enzyme; ss.
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AAQ75733 standard; DNA; 21
                                                                    (first entry)
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Gaps

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DB 1; Length 21; 1e+02; hes 0; Indels

Matches

à g

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AAQ75719;

AAQ75719,

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A method for the analysis of CDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE pliles AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                               Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                              Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 1; Length 21;
Pred. No. 1e+02;
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Matches 19; Conservative
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                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Analysis; gene expression; reverse transcription; primer; cDNA;
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                                  1.7%; Score 19; DB 1; Length 21;
100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
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                                                                                                        1082 TTAAAAAAAAAAAAA 1100
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                                                                       Conservative
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                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-018287/03.
                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                              AAQ75719 standard;
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AAQ75721

EXHXEXE

AAQ75721/c

RESULT 34

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Query Match

Matches

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Gaps

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A method for the analysis of cDNA comprises (a) preparing an anggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreasing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
Disclosure; Page 8; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rapidly and easily.
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Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

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Length 21;
                                0; Indels
 1.7%; Score 19; DB 1;
100.0%; Pred. No. 1e+02;
tive 0; Mismatches C
                                                     1082 TTAAAAAAAAAAAAA 1100
                              Conservative
               Similarity
                            19;
Query Match
Best Local (
                          Matches
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Gaps

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19 TTAAAAAAAAAAAAA 1 g

RESULT 37

ABK86168 standard; DNA; 24 24-SEP-2002 ABK86168; RESULT 36 ABK86168,

BP

(first entry)

Oligo dT primer #1 used in method to study gene expression.

Oligo dT primer; gene expression analysis; primer; ss.

Synthetic.

WO200236828-A2

10-MAY-2002

01-NOV-2001; 2001WO-US45401.

01-NOV-2000; 2000US-244933P.

(GENO-) GENOMIC SOLUTIONS INC.

Nagel AC;

Dombkowski AA,

Kane MD,

WPI; 2002-508123/54.

Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end ...

Disclosure; Page 11; 45pp; English.

The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that are expressed at different levels between 2 or more samples, where that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems are all systems are molecular or biochemical assay compositions and systems are linked to DNA or RNA comments. sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is

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0
not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences in mRNA level, to determine mRNA expression level and mRNA identification in one assay; (c) generates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology the genome of the organism under investigation and can be employed in organisms lacking significant genomic sequence in formation. The present sequence is sequenced in the method of the security sequence.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                Length 24;
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                                                                                                                                                                                                                                          Score 19; DB 1; Le:
Pred. No. 1.2e+02;
0; Mismatches 0;
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100.0%; Pred
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Best Local Similarity
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Oligo dT primer #2 used in method to study gene expression. Oligo dT primer; gene expression analysis; primer; ss. ABK86169 standard; DNA; 24 BP 01-NOV-2001; 2001WO-US45401. 01-NOV-2000; 2000US-244933P. 24-SEP-2002 (first entry) WO200236828-A2 10-MAY-2002 Synthetic.

Dombkowski AA, Nagel AC; (GENO-) GENOMIC SOLUTIONS INC. Kane MD,

WPI; 2002-508123/54.

Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end

Disclosure; Page 11; 45pp; English.

The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having a specific oligo-dT primer sequence, where the identimer comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where desired, for supporting discovery of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences

13-MAY~1998; 27-MAR-1998; Warthoe RESULT 38 AAV71935/c Matches 8\$\$\$\$\$\$\$\$\$\$\$\$ à 엄

in mRNA level, to determine mRNA expression level and mRNA identification in one assay; (c) generates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology techniques; and (d) does not require prior knowledge of the sequence of the genome of the organism under investigation and can be employed in organisms lacking significant genomic sequence in formation. The present sequence represents an oligo dT primer used in the method of the 1.7%; Score 19; DB 1; Length 24; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 other; 1082 TTAAAAAAAAAAAAA 1100 TTAAAAAAAAAAAAA 21 19; Conservative Similarity invention. Query Match Local

0

Gaps

0

AAV71935 standard; DNA; 27 BP. (first entry) 18-FEB-1999 AAV71935;

Anchored poly T RT-PCR primer.

Normalised; cDNA library; mRNA cloning; reverse transcription; immobilise; screening; hybridisation; nucleic acid amplification; expression pattern; drug development; PCR primer; RT-PCR; ss.

Synthetic.

WO9851789-A2

19-NOV-1998

98WO-DK00186.

98DK-0000432. 97DK-0000547. 97US-0871030. 13-MAY-1997; 19-MAY-1997; (DISP-) DISPLAY SYSTEMS BIOTECH APS

WPI; 1999-009772/01.

Preparation of normalised, subdivided cDNA libraries from mRNA - by reverse transcription and amplification, used to screen for new genes and interacting proteins, potential drugs, and for diagnosis

English. Example 1; Page 29; 71pp; The invention relates to preparation of a normalised, subdivided library of amplified cDNA from the coding regions of mRNA in a sample. The method involves reverse transcription, with at least one CDNA primer of formula 5.-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second cond and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second cond primer of a similar formula, in the presence of DNA polymerase I (or cond. PNA polymerase I (or cond. PNA polymerase I (or a database (a computer-spentated list of molecular weights of restricted a database (a computer-spentated list of molecular weights of restricted cond. PNA fragments of known sequence) is used to determine presence of an expressed protein in a cell, also to detect changes in such expression (particularly for diagnosis of disease). Surfaces (chip) having amplified cDNA stably immobilised on it, obtained by a similar method,

0 are used to screen for genes of a particular family, by hybridisation with nucleic acid from the family (to identify new genes) and to detect differences in expression patterns between cells. The polypeptides expressed by the libraries can be used for drug development. Sequences AAV71935 to AAV71946 represent primers used to exemplify the method of Gaps Primer; ss; DNA microarray; differential expression analysis; human. 0; Length 27; Indels 1.7%; Score 19; DB 1; Le 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 other; Jokhadze G, Bibilashvilli R; #80. 1082 TTAAAAAAAAAAAAA 1100 Human gene specific PCR primer BP. 27 TTAAAAAAAAAAAAAA 99US-0225928. 97US-0859998. ABK65992 standard; DNA; 27 02-JUL-2002 (first entry) Query Match
Best Local Similarity 100.
Matches 19; Conservative (CLON-) CLONTECH LAB INC. WPI; 2002-314699/35. Homo sapiens. US6352829-B1. 05-JAN-1999; 21-MAY-1997; Chenchik A, 05-MAR-2002 ABK65992; ABK65992/c 8.5666666 à d

Producing sub-population of labeled nucleic acids, useful for analysing differences in RNA profiles between several different physiological differences in RMA profiles between several different sources, using set of distinct gene specific primers

Example 3; SEQ ID No 80; 11pp; English.

acids (NAS) comprising contacting a NA sample from a physiological conditions to enzymatically generate sub-population of NAS, where each gene specific primers under suitable conditions to enzymatically generate sub-population of NAS, where each gene specific primer has a sequence complementary to a distinct mana, and each labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of labeled NAS which is useful for analysing the difference; where the method that which is useful for analysing the difference; where the method physiological sources, comprises producing subpopulation of labeled NAS for the different physiological sources in the populations for each physiological sources in the population, where the comparison is preferably performed by hybridising the labeled NAS for each of the distinct physiological sources in the population, where the comparison distinct physiological sources on a rray of probe NAS stably astociated with the surface of a substrate to produce a hybridisation pattern for each of the sources, and comparing the patterns for each of the sources, and comparing the patterns for each of the sources, and comparing the patterns for each of the sources, and comparing the patterns for each of the sources, and comparing the patterns for each of the sources, and comparing the patterns for each of the sources. Utilised in differential expression analysis of diseased a normal substrate types. The present sequence is a human gene specific PCR brimer used in the method of the invention. nucleic invention relates to producing a sub-population of labeled

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RESULT 40

qq à

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DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                        Nck associated protein 1; Napl; human; apoptosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein 1 (Napl) of the invention. Napl inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                Protein inhibiting apoptosis, useful in the diagnosis and treatment of Alzheimer's disease
        PCR primer for human Nck associated protein 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.7%; Score 18.6; DB 1;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 CAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 76; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC96240 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 rRNA gene PCR primer #207.
                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK.
(SAKA/) SAKAKI Y.
                                                                                                                                                                                                      98WO-JP05646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2000; 2000WO-EP03636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0303215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                         therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ulfendahl P, Wong K;
                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-395181/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-679677/66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200065088-A2.
                                                                                                       Homo sapiens.
                                                                                                                                      WO9931239-A1
                                                                                                                                                                                                      14-DEC-1998;
                                                                                                                                                                                                                                     15-DEC-1997;
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                                                                                                                                                                      24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-2000.
                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                   Sakaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC96240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of human cyclophilin-40-12.54. The sequences can be used in the treatment of immunopathy and cancer. The present sequence is a PCR primer for the coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 1.7%; Score 18.8; DB 1; Length 24; Local Similarity 90.9%; Pred. No. 1.36+02; nes 20; Conservative 0; Mismatches 2; Indels
                                               http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
                                                                                                          / Match 1.7%; Score 19; DB 1; Length 27; Local Similarity 81.5%; Pred. No. 1.3e+02; les 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Human cyclophilin-40-12-54 coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 17 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 other;
                                                                            Sequence 27 BP; 7 A; 8 C; 6 G; 6 T; 0 other;
                                                                                                                                                                           174 GCTGACAGTCACAGTGGCCGGGTCAGT 200
                                                                                                                                                                                                    27 GCAGACAGTCACTGGTTTGGTCAGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BODE-) BODE GENE DEV CO LTD SHANGHAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2000; 2000CN-0116823
                                                                                                                                                                                                                                                                                      AAL47515 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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ID AAX84258 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-305482/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CN1331162-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                                                                                                                                                                                                                                                                                                        AAL47515;
                                                                                                            Query Match
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Matches
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The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used to type the human leukocyte antigen genes (HLA) and 16s rRNA genes in particular.
                              classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel contiguous and partially overlapping CDNA sequences and their encoded polypeptides, designated PAIS3, transcribed from human pancreatic tissue and which have cytostatic activity. The PAIS3 polymucleotides, proteins and antibodies are all useful in methods of detection. Detection of PAIS3 polymucleotide, antigens or anti-PAIS3 antibodies in a sample is indicative of pancreatic disease. PAIS3 antibodies (antagonists) can also be used in vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours or metastases. Antisense PAIS3 polymucleotides can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pancreatic disease; PA153; human; cytostatic; detection; antigen; anti-PA153; antagonist; therapy; treatment; tumour; metastasis; gene therapy; EST; expressed sequence tag; primer; ss.
                                                                                                                                                                                                                                                                                                               1.7%; Score 18.6; DB 1; Length 25; 34.0%; Pred. No. 1.4e+02; Ive 0; Mismatches 4; Indels
                  Identifying extendible primers for use in identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pancreatic PA153 EST-specific clone primer 12
                                                                                                                                                                                                                                                                          Sequence 25 BP; 3 A; 4 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA153 cDNA transcribed from pancreatic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen M, Colpitts TL, se EN, Hodges SC, Klass tussell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                  1072 AAAGCAACTATTAAAAAAAAAAA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                   25 AAAGGAGGTATTCAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 121; 123pp; English
                                                                                                  Claim 14; Page 47; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts-Rapp L, Russell JC,
                                                                                                                                                                                                                                                                                                                                 84.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX78723 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.0
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-405041/34.
                                                                   of specific length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9931274-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX78723;
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BP

Kratochvil JD;

Friedman PN; MR, Kratoch

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therapy of pancreatic diseases. AAX78712-X78725 represent primers used in the method of the invention.
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĕ
                                                                                                                                                                                                                                                                                        BS124; breast; cancer; detection; diagnosis; prevention; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of an oligomucleotide used in the isolation o BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kratochvil JD;
                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 26;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman PN;
MR, Kratochv
H;
                                                            i, DB 1;
1.5e+02;
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                                                                                                                                                                                                                                                                  Human BS124 specific EST clone oligonucleotide.
                                  Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;
                                                         1.7%; Score 18.6; Dilarity 84.0%; Pred. No. 1.5e Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Billing-medel PA, Cohen M, Colpitts TL,
Gordon J, Granados EN, Hodges SC, Klass
                                                                                                         1076 CAACTATTAAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hodges SC, Kl
, Stroupe SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1076 CAACTATTAAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 97; 125pp; English.
                                                                                                                                26 Садавадарадарадарадара
                                                                                                                                                                                              BP.
                                                                                                                                                                                 7466/c
AAX07466 standard; cDNA; 26
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AAQ75597/c
ID AAQ75597 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         canados EN, H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-105623/09.
                                                                     Similarity
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                                                           / Ma.
Local S. ..
21;
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                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon J, G
Russell JC,
                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                   AAX07466;
                                                          Query Match
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                                                                                                                                                                                                                                                                                                         EST; BS.
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Matches
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S X C C
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQTS547-C75789) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                         CDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     in cDNA analysis technique.
                                                                                                                                                                                                                                     Score 18.4; DB 1; Length 20;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA and gene expression - by amplidigestion with restriction enzymes
                                                                                                                                                                                                           Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;
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                                                          Disclosure; Page 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                      1080 TATTAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                Reverse transcription primer used
                                                                                                                                                                                                                                                                                                            20 TATAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                     th 1.7%;
| Similarity 95.0%;
| 19; Conservative (
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ID AAQ75585 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                  Local Similarity
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                         Analysis of
followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP06303997-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis of
followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                AAQ75585;
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                               RESULT 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                  A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispersing each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                 Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                             cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression; reverse transcription; primer; cDNA;
                        Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 1.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                           (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                                                                  Page 5; 11pp; Japanese.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESER files AAQ75547-Q7578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispersing each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 1; Length 20; Pred. No. 1.2e+02;
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95.0%;
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Best Local Similarity
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amplification of mRNA

Matches

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AAQ75589;

AAQ75589/c

RESULT 48

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A method for the analysis of CDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSEDE plural type of labelled reverse transcription primers template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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95.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 1;
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Les 19; Conservative
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Best Local S
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AAQ75565/c
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          Gaps
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Pred. No. 1.2e+02;
0; Mismatches 1;
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   0; Mismatches
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Conservative
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Analysis followed

AAQ75577;

AAQ75577/c

RESULT 49

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Query Match

Synthetic.

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Gaps

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mENAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7798) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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followed by digestion with restriction enzymes
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ID AAQ75759 standard; DNA; 21
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             RESULT 52
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                and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digeting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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Best Local Similarity 95.0°
Matches 19; Conservative
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                                                                                                                           rapidly and easily
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AAQ75757;

AAQ75757/c

RESULT 51

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16-APR-1993;

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Query Match

Length 21; Indels rapidly and easily.

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEG files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dissting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                              ch 1.7%; Score 18.4; DB 1; Length 21; 1. Similarity 95.0%; Pred. No. 1.3e+02; 19; Conservative 0; Mismatches 1; Indels
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                                       (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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                                                                                                                                 Disclosure; Page 8; 11pp; Japanese.
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               93JP-0112515.
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                                                                 WPI; 1995-018287/03
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Best Local Similarity
              16-APR-1993;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESED files AAQ7554-705798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) dispesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression

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                              Length 21;
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                          1.7%; Score 18.4; DB 1;
95.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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95.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
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                                                                                1081 ATTAAAAAAAAAAAA 1100
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                                                       Conservative
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nes 19; Conservative
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                    Query Match
Best Local Similarity
Matches 19; Conserv
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AAQ75695 standard;
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Matches
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESS) files AAQ75547-07559 and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                         A method for the analysis of cDNA comprises (a) preparing an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
         CDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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Pred. No. 1.3e+02;
0; Mismatches 1;
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Pred. No. 1.3e+02;
0; Mismatches 1;
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                                                    Disclosure; Page 7; 11pp; Japanese.
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Matches 19; Conservative
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                                            expression; reverse transcription; primer; cDNA;
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             Reverse transcription primer used in cDNA analysis technique.
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                                                          aggregate; restriction enzyme; ss.
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Best Local Similarity
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription priners (GENESE) files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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Pred. No. 1.3e+02;
0; Mismatches 1;
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       1081 ATTABABABABABABA 1100
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and a plural type of labelled reverse transcription primers (GENBSEO files AAQ75547-Q75798) and using the aggregate of mRNAs as th template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                     rapidly and easily.
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Matches
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

Disclosure; Page 7; 11pp; Japanese.

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP

WPI; 1995-018287/03

93JP-0112515. 93JP-0112515,

16-APR-1993;

01-NOV-1994.

16-APR-1993;

JP06303997-A.

Synthetic.

Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

Reverse transcription primer used in cDNA analysis technique.

(first entry)

04-AUG-1995

AAQ75681;

BP.

AAQ75681 standard; DNA; 21

AAQ75681/c

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95.0%; Pred. No. 1.3e+02;
cive 0; Mismatches 1;
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1.7%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 1.3e+02; 1ive 0; Mismatches 1; Indels

1081 ATTARARARARARARA 1100

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AAQ75677/c
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                                                                                                                                   aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GBNESE) files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                               A method for the analysis of CDNA comprises (a) preparing an
                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                       (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                     Disclosure, Page 7; 11pp; Japanese.
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                                             WPI; 1995-018287/03
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                                                            Length 21;
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95.0%; Pred. No. 1.3e+02;
                                                    Score 18.4; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 1;
Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;
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                                                                                                                                                        1080 TATTAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggregate; restriction enzyme; ss.
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ID AAQ75629 standard; DNA; 21 BP.
                                                    1.7%;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNSSE) files AAQTSAT_QTSTAS) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75247-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                               1.7%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 1.3e+02; Live 0; Mismatches 1; Indels
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       followed by digestion with restriction enzymes
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                                                                                                                                                                                                                   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
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                                     Disclosure; Page 6; 11pp; Japanese.
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; restriction enzyme; ss.
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                               expression; reverse transcription; primer; cDNA;
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 Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 1.3e+02; 1ve 0; Mismatches 1; Indels
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                                              restriction enzyme; ss
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AAQ75631 standard; DNA;
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Best Local 9
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Matches
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The present invention describes a method for the comparative detection of the amount of an RNA. The method comprises: (a) cDNAs obtained by transcribing respectively from at least two tissue RNAs are respectively fragmented by using a same restriction enzyme; (b) each different adaptor and a common adaptor are added to each of the cDNA fragments derived from the same or different tissues by the step (a); (c) the resultant adaptor-added cDNAs are mixed together; (d) an adaptor primer having the common sequence to said different adaptor—added cDNAs containing no region derived from to amplify said adaptor—added cDNAs containing no region derived from colyadenylic acid of the mRNA before the addition of the adaptor among the adaptor—added cDNAs prepared by the step (b); (e) the ratios of the cDNA amounts are measured between the tissues; (f) the RNA is detected cf rom the measured result; (g) each different adaptor and a common adaptor are added to each of the genomic DNA fragments derived from a same or different individuals; (h) the resultant adaptor—added genomic DNAs are mixed together; (i) the adaptor—added genomic DNAs are amplified by using an adaptor primer having the common sequence to the different adaptor and a captor common sequence to the different adaptor and a sequence—specific adaptor; and (j) the ratios of the amplified amounts of the genomic DNAs are measured between the individuals. The method is used for the detection of the amounts of RNA and DNA. The present consequence represents an oligonucleotide which is used in the reemplement.
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anti-HIV; PCR; primer; ss.
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                                                                                                                                                                                                                                                Comparative detection of the amounts of RNA and DNA -
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                                                                                                                 30-MAY-2000; 2000JP-0160324.
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                                                                                                                                                            (UNIT-) UNITECH CO
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Best Local Similarity
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                               04-DEC-2001.
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                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                                                                                                                                                                                                               expression; reverse transcription; primer; cDNA;
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1081 ATTAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                 aggregate; restriction enzyme; ss.
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                                           20 АТСАААААААААААААА
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AAQ75634 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                        Analysis; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2001333800-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TP06303997-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L6-APR-1993;
                                                                                                                                                                                                                                       04-AUG-1995
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19;

Best Loca Matches

Query Match

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RESULT 71

ABA93238

ABA93238;

Synthetic

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Gaps

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1079 CTATTAAAAAAAAAAA 1098
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                                                                                                                                                                                                                                                                                                                                                                       5 CTCTTAAAAAAAAAAAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH76998 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                Local Similarity
les 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mao Y, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH76998;
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                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH76998/c
                                                                                                                                                                                                                                                                                                              datches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; nucerlar dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatooid arthritis; multiple solerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The
                                                                       human zinc finger protein 9.79 polypeptide, useful for treating diseases e.g. cancer and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e, useful for detecting the presence, polynucleotide polymorphism in a nucleic
                                                                                                                                         The present invention relates to human zinc finger protein 9.79 (see ABPS9011). The zinc finger protein is useful for treating several diseases e.g. cancer and HIV infection. The present sequence is a PCR primer, which was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                              1.7%; Score 18.4; DB 1; Length 24; 95.0%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels
                                                                                                              Example 2; Page 16 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                 Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP specific SNPE primer SEQ ID 2755.
                                                                                                                                                                                                                                                                                                     1081 ATTAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                    23 ATGAAAAAAAAAAAAAAA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genotyping oligonucleotide, absence or identity of single po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Σ
                                                                                                                                                                                                                                                                                                                                                                                                        AAH39959 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                       human zinc finger
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohl
                                          WPI; 2002-548879/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-290930/30.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Picoult-Newburg L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200129262-A2.
               Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH39959;
                                                                       A novel
                                                                                    several
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               Mao
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AAH39959
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oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples. for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinamia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesteroleemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, concern anaetion, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide comment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    applicable in diagnosis and treatment of cancer, hemopathy, human immunodeficiency virus infection, immunological diseases and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human amyloid precursor protein 9 and encoded polynucleotide,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, amyloid precursor protein 9; recombinant production, malignant tumour, cancer, blood disease, HIV infection, human immunodeficiency virus; immune disorder; inflammatory cytosteatic, anti-HIV; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%; Score 18.4; DB 1;
95.0%; Pred. No. 1.5e+02;
Ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 16 A; 2 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
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Gaps

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treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAAH76997-AAH76998 represent reverse transcription-PCR (RT-PCR) primers used in an exemplification of the invention to isolate human amyloid precursor protein 9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such a class 1/2 HLA comprises identifying all possible nucleotide sequences of specific length
 and nucleotides which encode it may be used for
                                                                                                                                                                                                                                                Length 24;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                          Query Match
1.7%; Score 18.2; DB 1;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3;
                                                                                                                                                                                                      Sequence 24 BP; 1 A; 1 C; 4 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                     1078 ACTATTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
                                                                                                                                                                                                                                                                                                                                                        23 ACCCGTAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 44; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16s rRNA gene PCR primer #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2000; 2000WO-EP03636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC96060 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong K;
 precursor protein 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-679677/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200065088-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC96060;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 75
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receiver, and to identify bacteria in a sample. The method can be used to type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences of specific length.
                                                                                                                                                                                                                   DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a method for identifying a set of extendible primers which can be used in the identification. Fyping and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.7%; Score 18.2; DB 1;
87.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 4 A; 2 C; 4 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anchored poly(T) oligonucleotide polyT-AnchA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
1076 CAACTATTAAAAAAAAAAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1073 AAGCAACTATTAAAAAAAAA 1095
                             23 CAGCGTTTAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AAGCTACTTCTAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 45; 66pp; English.
                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                          16s rRNA gene PCR primer #52.
                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000; 2000WO-EP03636.
                                                                                                   AAC96085 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT94667 standard; DNA; 18
                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ulfendahl P, Wong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-679677/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                          WO200065088-A2.
                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                AAC96085;
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ID AAT946
                                                                                     AAC96085/
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Length 25;

1.7%; Score 18.2; DB 1; 87.0%; Pred. No. 1.7e+02; rative 0; Mismatches 3;

20; Conservative

Best Local Similarity

Matches

Query Match

Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 other;

t C

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-M3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or cytosine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for FP-PCR and determination of base sequences. The new sequences allow for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-0759) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                  reproductive and highly efficient analysis of gene sequences.
                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                            DB 1; Lens.
                                                                                                                                                                                                                                                                                      Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                1.6%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
Disclosure; Page 11; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       1082 TTAAAAAAAAAAAA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                           18 TTAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ75553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 79
AAQ75553/c
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                                                                                                                                                                                                                                                                                                                                                                                                                         Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream region of a polyadenylation sequence. They were used to prime cDNA synthesis from sangdragon (Antirrhinum majus) petal and leaf RNA, and were also utilised in the PCR amplification of plant cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see using a differential display approach. This can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides having at least two new nucleotides - useful as primers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                            Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 1.3e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 manipulate the pigmentation of transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT-PCR primer of the invention SEQ ID 13.
                                                                                                                                                                                                                                          Michael MZ
                                                                                                                                                                                                                                                                                                                                                                                         Example 15; Page 59; 234pp; English.
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                                                                                                                          97WO-AU00124
                                                                                                                                                            96AU-0008386
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1es 18; Conservative
                                                                                                                                                                                                                                        Brugliera F, Holton TA,
                                                                                                                                                                                                  (FLOR-) FLORIGENE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKI ) TAKARA SHUZO
                                                                                                                                                                                                                                                                          WPI; 1997-448691/41.
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                                            WO9732023-A1
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          Synthetic.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVIS4T-QTS78) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to create transgenic plants with altered petal colour
                                                                                                                                                                                                               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6%; Score 18; DB 1; Length 19; 0.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome P450 sequence amplification PCR primer polyT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ....
                                                                                                                                             NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants; altered petal colour; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                               Disclosure; Page 5; 11pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1083 TAAAAAAAAAAAAA 1100
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                                                                                93JP-0112515
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93AU-0006698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     rapidly and easily.
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             JP06303997-A.
                                                                              16-APR-1993;
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07-JAN-1993;
                                             01-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1994
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Matches
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AAQ49436/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEG files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                                                                                                                                                                                                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                      Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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        1083 TAAAAAAAAAAAAA 1100
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                                        18 TAAAAAAAAAAAA 1
                                                                                                                      AAQ75554 standard; DNA; 19 BP
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by
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                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                        AAQ75554;
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followed
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AAQ75586;
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AAQ75586/c
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Onn-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally curring SCF, stimulate growth of primitive progenitors such as memacopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow centrality after chemotherapy or radiation-induced bone marrow aplasia or myelosupression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells
                                                                                                                                                                                                                                                                                                                  Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
                      The sequence is that of a PCR primer which was used in polymerase chain reactions for the amplification of cloned cytochrome P450
                                                                                                                                                                                                                                                                                                                                          Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.
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0
                                                                                                           Length 20;
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                                                                                                      1.6%; Score 18; DB 1; I
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
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                                                           field.)
                                                                               Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
                                                      Updated on 25-MAR-2003 to correct PN
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Disclosure; Page 25; 86pp; English.
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                                                                                                                                                    1083 TAAAAAAAAAAAAA 1100
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89US-0422383.
90US-0537198.
90US-0573616.
90WO-US05548.
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                                                                                                                                                                                                                                                                                  (updated)
(first entry)
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                                                                                                                               18; Conservative
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                                                                                                                 Best Local Similarity
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15-MAY-1996
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16-OCT-1989;
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the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                              Length 20;
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
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tive 0; Mismatches
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Les 18; Conserv
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                       Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                       digestion with restriction enzymes
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         (first entry)
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                                                aggregate;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreship the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                      aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as th template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                     the analysis of cDNA comprises (a) preparing an double-stranded cDNAs by using an aggregate of mRNAs
                                     cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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restriction enzyme; ss.
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1 Similarity 100.0%; Pred. No. 1.4e+02;
18; Conservative 0; Mismatches 0;
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Best Local Similarity
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followed by
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                                                                                       gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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Pred. No. 1.4e+02;
0; Mismatches 0; Indels
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Length 20;

Score 18; DB 1;

1.68;

Query Match

Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;

0;

RESULT 88

AAQ75590/

Best Loc Matches

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AAQ75590;

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                    Gaps
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Pred. No. 1.4e+02;
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Mismatches 0;
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100.0%; Pic
                                                           1083 TAAAAAAAAAAAAAA 1100
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                                                                                                                                                                          AAQ75590 standard; DNA; 20
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                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                           Conservative
            Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NITE ) NIPPON
                                                                                                                                                                                                                                          04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            L6-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1993;
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04-AUG-1995

AAQ75575;

1083

à DP

Query Match

Matches

18

RESULT 89 AAQ75575,

11-NOV-1994.

Synthetic

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Gaps

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Indels

mRNA

Phosphorothioate oligonucleotide

07-DEC-1998

AAV07752;

AAV07752 standard; DNA; 20 BP

RESULT

us09904568-1.rng

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A method for the analysis of cDNA comprises (a) preparing an anggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESER files AAQ75547-Q7578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                             ch 1.6%; Score 18; DB 1; Length 20; l Similarity 100.0%; Pred. No. 1.4e+02; 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                         Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                               1083 TAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                 TAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                  AAQ75578 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0112515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                        rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                             Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ75578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis
followed
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                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 91
AA075578/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                       phosphorothioate; sulphurisation; heterocycle; automated synthesis; antisense; EDITH; Beaucage reagent; ss.
                                                                                                                                                                                                    /*tag= a
/note= "phosphorothioate internucleotide linkages"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulphurisation of phosphorus-containing compounds, e.g. oligo:nucleotide(s) - by contacting the compound with a di:sulphide-containing five-membered heterocycle
                                                                                                                                                                                                                                                                                                                                                                                               X
                                                                                                                                                                                                                                                                                                                                                                                               Musier-Forsyth K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 1 A; 0 C; 0 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                    LOUISIANA STATE & AGRIC,
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 30; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 TAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                          Hammer RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e
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                                                                                                                                                                                                                                                                                                 97WO-US07118.
                                                                                                                                                                                                                                                                                                                           96US-0641920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA13753 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                         1..20
/*tag=
                                                                                                                                                                                                                                                                                                                                                 (LOUU ) UNIV LOUISIANA (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-549671/50.
                                                                                                                                                                                                                                                                                                                                                                                            Chen L,
                                                                                                                                                                         Key
misc_feature
                                                                                                                                                                                                                                          WO9741130-A2.
                                                                                                                                                                                                                                                                                             29-APR-1997;
                                                                                                                                                                                                                                                                                                                        30-APR-1996;
                                                                                                                                                                                                                                                                    06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-2000
                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          Barany G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA13753;
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δ
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Gaps

0;

100.0%; Prative 0;

18; Conservative

Matches

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Local Similarity

1083 TAAAAAAAAAAAAA 1100

ТААААААААААААА 1

8 16:51:41 2004

Thu Jan

24-OCT-2001 (first entry)

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Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
               Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia;
Stem cell factor universal oligonucleotide 220-7.
                                                                                                                                                                                                               Bosselmann RA,
                                                                                                                                                                                                                                                                             Example 3; Fig 12C; 123pp; English.
                                                                                                                                   89US-0422383.
90US-0537198.
90US-0573616.
90WO-US05548.
                                                                                                                    99EP-0122861,
                                                                                                                                                                    90US-0589701
                                                                                                                                                                                                              Suggs SV,
                                                                                                                                                                                                                             WPI; 2000-259135/23.
                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                   04-OCT-1990;
                                                                                                                                                                            04-OCT-1990;
                                                                                   EP992579-A1.
                                                                                                                                    16-OCT-1989
                                                                                                                                           11-JUN-1990;
                                                                                                                                                            28-SEP-1990;
                                                                                                   12-APR-2000
                                                                                                                                                                    01-OCT-1990
                                                  cancer; ss
                                                                                                                                                                                                            Zsebo KM,
                                                                                                                                                                                                                                                              factor
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Martin FH;

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A method has been developed of making haematopoietic cells suitable for administration to a subject. The method comprises: (a) obtaining the haematopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a colls by adding to the cells a haematopoietically effective dose of a confirmation and one or more of the biological properties of naturally occurring stem cell factor (SCF). The method is useful for stimulating cells which are capable of maturing to erythroid, megakaryocyte, or primitive progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic disorders. The method is useful for treating haematopoietic progenitors in syngeneic, enhancing the efficiency of gene therapy based on transfecting contample stem cells. SCF is also useful for combating the myelosuppressive effects of anti-HIV drugs such as Aboost to the myelosuppressive effects of anti-HIV drugs such as a boost to the myelosuptic system for fighting neoplasia (cancer). The present sequence the nexample from the represents a universal oligonucleotide which is used in an example from
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0
                                                                        Gaps
                                                                        ·,
                                1.6%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                18; Conservative
                                               Local Similarity
                                Query Match
                                               Best Loca
Matches
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1083 TAAAAAAAAAAAAA 1100
                               TAAAAAAAAAAAAA 2
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셤 à

1083 TAAAAAAAAAAAAAA 1100 TAAAAAAAAAAAAAA 2

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AAH41332 standard; DNA; 20

RESULT 95 AAH41332/c

AAH41332;

BXXX

AAS10448 standard; DNA; 20 AAS10448; RESULT 94
AAS10448/C
ID AAS1044
XX
AC AAS1044

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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence for universal PCR primer 220-7 is 1 of 19 PCR primers (AAS10435-AAS10453) used to amplify various portions of the human SCF CDNA sequence. The sequence is described in an invention relating to novel stem cell factors, the polynucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor effective human peripheral blood by administering a haematopoietically effective human stem cell factor polypeptide. The methods are useful for myelosclerosis, osteopetrosis, including myelofibrosis, myelosclerosis, metastatic carcinoma, acut; leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS.
                                                                             Human, stem cell factor, SCF, haematopoietic progenitor cell;
blood disorder, Hodgkin's disease, vitamin B12; folic acid deficiency,
hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increasing the number of early haematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                             Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 18; DB 1; Length 20; 00.0%; Pred. No. 1.4e+02; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 100.0%; Pred. No. 1.4
18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 12C; 210pp; English.
                                                                                                                                                                                                                                                                                            92US-0982255.
                                                                                                                                                                                                                                                                                                                            90US-0537198.
                                                                                                                                                                                                                                              95US-0449653
                                                                                                                                                                                                                                                                                                                                                                         93US-0172329
                                                                                                                                                                                                                                                                                                                                                            90US-0589701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                        ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                          25-NOV-1992;
16-OCT-1989;
11-JUN-1990;
                                                                                                                                                                              US6248319-B1
                                                                                                                                                                                                                                           24-MAY-1995;
                                                                                                                                                                                                            19-JUN-2001.
                                                                                                                                                                                                                                                                           10-APR-1991;
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01-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                          (ZSEB/)
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21-AUG-2001 (first entry)

us09904568-1.rng

PCR primer; ss.

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95US-0482918
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                           BOSSELMAN R A. SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-298941/31.
                                                                                                                                                                                                                                                                                                                                                                                                   (MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                  SUGGS S
                                                                                                                                                                                                                                                                                                                                         ZSEBO
                                                       Homo sapiens.
                                                                                                                                                                                                                                     16-OCT-1989;
11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
                                                                                            US6207417-B1
                                                                                                                                                                           07-JUN-1995;
                                                                                                                                  27-MAR-2001.
                                                                                                                                                                                                                 21-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS04213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                           (BOSS/).
(SUGG/)
                                                                                                                                                                                                                                                                                                                                         ZSEB/)
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            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for enhancing (B) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCF) receptor to a biologically active SCF, its analogue or fragment, which induces cell prohiferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. AAH41301 to AAH41364 and AAB9831S1 to AAB983390 represent sequences used in the exemplification
                                                                             Stem cell factor; SCF; stem cell factor receptor; blood cell disorder; gene therapy; PCR primer; mutagenesis; probe; ss.
                                      Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymucleotide into cell in vitro -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 12C; 210pp; English.
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89US-0422383.
90US-0537198.
90US-0573616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-366062/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN
                                                                                                                                                                                   US6207454~B1
                                                                                                                                                                                                                                                                                                                          24-MAY-1995;
12-JAN-1998;
25-NOV-1992;
                                                                                                                                                                                                                                                                   31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1990;
01-OCT-1990;
                                                                                                                                                                                                                            27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-1989
                                                                                                                                                                                                                                                                                                         21-DEC-1993
                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS04112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 96
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NAMES OF COLORS OF STREET AND STR
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Martin FH;

Suggs SV,

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The present sequence for universal PCR primer 220-7 is 1 of 8
universal oligonucleotides (AASO4110-AASO4117) used in the
isolation of the human SCF (stem cell factors condition to the human SCF (stem cell factors) cDNA sequence. The
present invention relates to novel stem cell factors
(AAU02453-AAU02458, AAU02460, AAU02461) and the polymucleotides
encoding them. SCF stimulate primitive progenitor cells including early
hamatopoietic progenitor cells. The invention also describes SCF
peptides (AAU02462-AAU02481) and the oligonucleotides
(AASO4081-AASO4011) used in the isolation of human and rat SCF
sequences. The polymucleotide encoding SCF is useful for producing SCF
and useful in gene therapy. It is useful for treating disorders
involving blood cells such as myelofibrosis, metastatic carcinoma,
caute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
daucher's disease, anaemia, congestive splenomegaly, Kala azar,
sarcoidosis, military tuberculosis, disseminated fungus disease,
sarcoidosis, military tuberculosis, disseminated fungus disease,
Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
piebaldism and vitiligo.
Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's disease, Kala azar, anaemia and septicemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 18; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                       Example 3; Fig 12C; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1083 TAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 18; Conservative
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Homo sapiens
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universal oligonucleotides (AASO4218) used in the
isolation of the human SCF (stem cell factor) cDNA sequence. The
present invention relates to novel stem cell factors

(AAU02761-AAU02767-AAU02775, AAU02797) and the polynucleotides
encoding them. SCF stimulater primitive progenitor cells including early
haematopoietic progenitor cells. The invention also describes SCF
(AASO4182-AASO4210) used in the isolation of human and rat SCF
sequences. The polynucleotide encoding SCF is useful for producing SCF
and useful in gene therapy. It is useful for treating disorders
involving blood cells such as myelofibrosis, metastatic carcinoma,
acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
cute leukaemia military tuberculosis, disseminated fungus disease,
bulminating septicemia, malazia, vitamin B12 and folic acid deficiency,
pyridoxine deficiency, and hypopigmentation disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                          Isolated DNA sequence, encoding polypeptide product useful for
                                                                                                                                                                                                                                                                        stimulating growth of early haematopoietic progenitor cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Bosselman RA, Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                           Example 3; Fig 12C; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1083 TAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH23890 standard; DNA; 20 BP.
                                                                                                                      92US-0982255.
89US-0422383.
90US-0537198.
90US-0573616.
                                                                                                   93US-0172329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyridoxine deficiency, ar
piebaldism and vitiligo.
                                                                                                                                                                                                                                      WPI; 2001-281051/29.
                                                                                                                                                                                          (AMGE-) AMGEN INC.
         PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; ss.
                                 Homo sapiens.
                                                      JS6218148-B1
                                                                                                 21-DEC-1993;
                                                                                                                                                         24-AUG-1990;
01-OCT-1990;
                                                                                                                                   6-OCT-1989;
                                                                                                                        25-NOV-1992;
                                                                                                                                              12-NUL-1390;
                                                                             .7-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-2001
                                                                                                                                                                                                                 Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH23890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH23890/c
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The present sequence for universal PCR primer 220-7 is 1 of 8
universal oligonucleotides (AAH23888-AAH23895) used in the
isolation of the human SCF (stem cell factor) cDNA sequence. The
present invention relates to novel stem cell factors

(AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
encoding them. SCF stimulates primitive progenitor cells including early
nematopoletic progenitor cells. The invention also describes SCF
peptides (AAB73578-AAB73597) and the oligonucleotides
(AAH23889-AAH23889) used in the isolation of human and rat SCF
sequences. The polynucleotide encoding SCF is useful for producing SCF
and useful in gene therapy. It is useful for treating disorders
involving blood cells such as myelofibrosis, metastatic carcinoma,
cute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
Gaucher's disease, anaemia, congestive splenomegally, Kala azar,
cute leukaemia, military tuberculosis, disseminated fungus disease,
sarcoldosis, military tuberculosis, disseminated fungus disease,
pyridoxine deficiancy, and hypopigmentation disorders such as
presentations and vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New stem cell factor polypeptides and their analogs which stimulate
growth of early hematopoietic progenitors, useful for treating aplastic
anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 18; DB 1; Length 20;
100.0%; Pred. No. 1.4e+02;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian stem cell factor PCR primer SEQ ID NO: 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.6%; Score 18; DB :
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 12C; 166pp; English.
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ID AAF89092 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 TAAAAAAAAAAAAA 2
                                                                                                                                                                                                   91US-0684535.
89US-0422383.
90US-0537198.
90US-0573616.
                                                                                                                                         92US-0982255
                                                                                                                                                                                                                                                                                                                                                   90US-0589701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-256683/26.
                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
US6204363-B1
                                                                                                                                                                                                                                                                                                                                                01-OCT-1990;
                                                                                                                                     25-NOV-1992;
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                                                                                                                                                                                                                                          16-OCT-1989;
11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-2001
                                                                    20-MAR-2001
                                                                                                                                                                                                                                                                                                                   24-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 99
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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFs). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemaglobinuria, malaria, pigentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention.
                                                                                                                                                                                                                                                                                       Novel isolated non-human mammalian stem cell factor polypeptide
stimulating growth of early haematopoietic progenitor cells, useful for
treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 12C; 209pp; English
                                                                                                                       89US-0422383.
90US-0537198.
90US-0573616.
90US-0589701.
                                                                            94US-033672B
                                                                                                         92US-0982255
                                                                                                                                                                                                                              Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          WPI; 2001-353108/37.
                                                                                                                                                                                                  INC.
                                                                                                                                                                                                 (AMGE-) AMGEN
                 US6207802-B1
                                                                           09-NOV-1994;
                                                                                                                                                    24-AUG-1990;
01-OCT-1990;
                                                                                                                       16-0CT-1989;
                                                                                                         25-NOV-1992;
                                              27-MAR-2001
                                                                                                                                                                                                                                                                                                                                       sarcoidosis
                                                                                                                                                                                                                               Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Suggs SV, Martin FH

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Score 18; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 0; Indels
               L Similarity 100,0%; Pred. No. 1.4
18; Conservative 0; Mismatches
                                                                  1083 TAAAAAAAAAAAAA 1100
     1.6%;
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TAAAAAAAAAAAAAA 2 13 Пр

SCF universal oligonucleotide 220-7. ABS73849 standard; DNA; 20 05-DEC-2002 (first entry) ABS73849; RESULT 100 ABS73849/c

Stem cell factor; SCF; blood-forming system; blood cell disorder; haemacopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Rodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antifungal; antimalarial; dermatological; ss.

Synthetic.

EP1241258-A2

18-SEP-2002

04-OCT-1990; 2002EP-0008587.

89US-0422383. 16-OCT-1989;

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90US-0537198.
90US-0573616.
90WO-US05548.
90US-0589701.
90EP-0310899.
   24-AUG-1990;
28-SEP-1990;
01-OCT-1990;
               04-OCT-1990;
            04-OCT-1990
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(AMGE-) AMGEN INC.

Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

WPI; 2002-684093/74.

Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukaemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA encoding the human SCF

Example 3; Fig 12C; 120pp; English.

The present invention relates to novel stem cell factors (SCFs), polynucleotide sequences encoding the SCFs, and methods of producing them. SCFs are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, multiples to the present sequence representing a universal oligonucleotide for SCF DNA is used in the examples of the present invention.

Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

; 0 Length 20; 0; Indels Query Match
1.6%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0;

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Gaps

1083 TAAAAAAAAAAAAA 1100 19 TAAAAAAAAAAAA 2 à 셤

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Gaps

AAD35465 standard; DNA; 20 BP. AAD35465,

RESULT 101

(first entry) 25-JUL-2002

AAD35465;

Rat SCF 5' cDNA amplifying PCR primer, 220-7.

Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; oli Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia; disseminated fungus disease; Fulminating septicaemia; pibbaldism; AIDS; acquired inmune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; biamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR; primer; ss

Rattus sp.

14-FEB-2002.

12-JAN-1998;

US2002018763-A1.

98US-0005243.

95US-0449653

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The Piezell. Libration relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally occurring SCF to allow possession of heamstopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopeania, thrombookytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, corresponding to the operation of the invention of the operation of operation of the operation of operations o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel non-naturally-occurring stem cell
                                                                                                                                                                                                                                                                                                                                           Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 12C; 217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the invention
                                                                            ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                       WPI; 2002-350789/38.
                                                                                                                                                                  MART/) MARTIN F H.
                        24-MAY-1995;
                                                                                                                                                                                                                             Zsebo KM,
                                                                            (ZSEB/)
(BOSS/)
                                                                                                                                          SUGG/)
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression

Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

Disclosure, Page 7; 11pp; Japanese.

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP

WPI; 1995-018287/03.

Martin FH;

Suggs SV,

Bosselman RA,

93JP-0112515. 93JP-0112515.

16-APR-1993; 16-APR-1993;

> . 0 1.6%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other; 1 Similarity 100.0%; Pred. No. 1.4 18; Conservative 0; Mismatches Query Match Best Local Similarity Matches à

1083 TAAAAAAAAAAAAA 1100 19 TAAAAAAAAAAAAA d

RESULT 102 AAQ75691/

AAQ75691 standard; DNA; 21 BP.

AAQ75691;

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

Synthetic

JP06303997-A.

01-NOV-1994.

Analysis; 0 Gaps (first entry) 04-AUG-1995

ö A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction Gaps 0 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes expression; reverse transcription; primer; cDNA; Reverse transcription primer used in cDNA analysis technique. 1.6%; Score 18; DB 1; Length 21; 100.0%; Pred. No. 1.5e+02; 0; Indels Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other; 100.0%; Prea. w.. (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. Disclosure; Page 7; 11pp; Japanese. aggregate; restriction enzyme; ss. 1083 TAAAAAAAAAAAAA 1100 AAQ75692 standard; DNA; 21 BP. 18 TAAAAAAAAAAAAA 1 93JP-0112515, 93JP-0112515 (first entry) Local Similarity 100. rapidly and easily. WPI; 1995-018287/03. JP06303997-A. 16-APR-1993; 16-APR-1993; 04-AUG-1995 01-NOV-1994 Query Match AAQ75692; RESULT 103 Matches AAQ75692, ð

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophorealing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
                                                                                               gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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                                                             Reverse transcription primer used in cDNA analysis technique.
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ive 0; Mismatches 0;
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enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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ive 0; Mismatches 0; Indels
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ7554798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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followed by digestion with restriction enzymes
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tive 0; Mismatches 0;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQTS47-QY5798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
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iive 0; Mismatches 0;
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RESULT 113

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A method for the analysis of CDNA comprises (a) preparing an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                         Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                         Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 18; Conservative
04-AUG-1995 (first entry)
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Pred. No. 1.5e+02;
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                                                       Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
                                                                                                         100.0%; Pred. No. 1.
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Best Local Similarity
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               seperate lanes.
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followed by
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AAQ75709

AAQ75709/ ID AAQ7 XX AC AAQ7 XX

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Gaps

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Mismatches

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Conservative

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Matches

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEO inles AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                           A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNSSEQ files AAQ75547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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              cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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                                                                Disclosure, Page 7; 11pp; Japanese.
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(first entry)

expression; reverse transcription; primer; cDNA;

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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                                                                                             standard; DNA;
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AAQ75716
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Length 21; Indels

Score 18; DB 1; Le Pred. No. 1.5e+02; 0; Mismatches 0;

1.6%; SCC_ 100.0%; Pre

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Length 21;

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Query Match Best Local Similarity

Synthetic.

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers and a plural type of labelled reverse transcription primers template for each reverse transcription prime; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 18; Conservative
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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Pred. No. 1.5e+02;
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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Best Local Similarity
Matches 18; Conserv
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Analysis;

AAQ75684

AAQ75684/c

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                           A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                              cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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Pred. No. 1.5e+02;
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Nes 18; Conservative
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                16-APR-1993;
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                                                                                                                                    Analysis of followed by
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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18

RESULT 124

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Query Match

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q75789) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzywe and; (c) electrophoreaing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                 amplification of mRNA
                                              gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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                     Reverse transcription primer used in cDNA analysis technique
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Pred. No. 1.5e+02;
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followed by digestion with restriction enzymes
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3. 1.5e+02; Indels
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rapidly and easily.
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Analysis followed

AAQ75688

AAQ75688/c ID AAQ7568 XX AC AAQ7568 XX DT 04-AUG-

RESULT 127

Query Match

Best Loca Matches

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aggregate; Synthetic

AAQ75687

RESULT 126

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQT)547-07798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the propared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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   cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                           Length 21;
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                                                                                                                                                                                                                                                    Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
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                                               Disclosure; Page 7; 11pp; Japanese.
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Matches 18: Consemination
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Analysis of
followed by
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                               restriction enzyme; ss.
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1083 TAAAAAAAAAAAAAA 1100
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                                                                                           AAQ75671 standard; DNA; 21
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Best Local Similarity
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AAQ75672/c
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   JP06303997-A.
               16-APR-1993;
                                       of
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        01-NOV-1994.
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(GENESEQ files FAQ75547-Q75798) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                      1.6%; Score 18; DB 1; Length 21;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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    a plural type of labelled reverse transcription
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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followed by digestion with restriction enzymes
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RESULT 134

A method for the analysis of CDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs

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Best Local Similarity
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17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ30431;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ30431
                           8888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X L L L X X X X X X X X X X B X B X X B X X B X X B X B X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
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                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/mod_base= CTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
12..23
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                                                                                                                                                                                        Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
                                                                                                                                                                                                                                          Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;
RSV; HPV; malignancy; hepatitis; inflammation; ss.
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/note= "o-xyloso dimer synthon linkage"
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|label= inverted_polarity_region
|note= "see_comments"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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AAQ30430/c
ID AAQ30430 standard; DNA; 23 BP.
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91US-0643382.
91US-0683420.
91US-0686544.
91US-0686547.
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                                                                                                                       (updated)
(first entry)
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modified_base
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17-APR-1991;
17-APR-1991;
27-SEP-1991;
                                                                                                                       25-MAR-2003
07-DEC-1992
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08-APR-1991;
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Gaps
the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as varified by in vitro systems. See also AAQ22452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-6 gene, herpes simplex; AIDS; modified; HIV;
RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                       Length 23;
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/note= "o-xyloso dimer synthon linkage"
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/mod_base= CTHER
/note= "OTHER= N4 N4 ethanocytosine"
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                                                                                                                                                                          1.6%; Score 18; DB 1; Le
100.0%; Pred. No. 1.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= inverted polarity_region
/note= "see comments"
11..12
                                                                                                                       Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 other;
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2 TAAAAAAAAAAAAA 19
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                                                                                                                                                                                                                                                                                                                                1083 TAAAAAAAAAAAAAAAA
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ses 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                     nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV42215;
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 137
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                               AAV42215,
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                     The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand configurations. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant than assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso formed from an o-xyloso dimer synthon. The linking gp is o-xyloso conditions. The oligomer tatable to mucleotides are coupled through a xylone residue to form the dimer synthon. This additional modifications may render the oligomer stable to mucleotides are coupled through a xylone residue the oligomer stable to muclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. Cupdated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a variant human MLH1 or MSH2 gene. Also described are: (1) a method for diagnosing or predicting susceptibility to hereditary non-polyposis colorectal cancer (HNPCC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the human MLH1 and MSH2 genes for diagnosing or determining a predisposition for hereditary non-polyposis colorectal
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC; hereditary non-polyposis colorectal cancer; ds.
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                   Score 18; DB 1; Length 23; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                100.0%; Preu. ... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             1083 TAAAAAAAAAAAAAA 1100
    Claim 12; Page 71; 77pp; English.
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LING/) LING J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2001044936-A1.
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comprising screening a DNA sample for the variant MLH1 or MSH2 gene where presence of the variant indicates presence of, or susceptibility to TNPCC; (2) a method of identifying mutants in splice donor or acceptor sites of a human MLH1 gene, comprising sequencing splice donor or or acceptor sites of the gene with intronic primers for the human MLH1 confidentifying mutants in splice donor or acceptor sites of a human MSH2 gene, comprising sequencing splice donor or acceptor sites of the gene with intronic primers for the human MSH2 gene and analysing the sequence confidentify any witherstep; and (4) a transgenic model system for to identify any mutants; and (4) a transgenic model system for colorectal cancer comprising cells expressing the variant MLH1 or MSH2 colorectal cancer comprising cells expressing the variant MLH1 or MSH2 colorectal cancer. The hMLH1 and hMSH2 variants are used to diagnose or determine a patients succeptibility to heredicary non-polyposis colorectal cancer. ABL01648 to ABL01745 and ABL01745 to ABL01831 represent hMLH1 and hMSH2 confident invention. ABL01832 to ABL01839 confidential cancer comprising cells expressent mutagenic primers used in the exemplification of the present
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note= "labelled with the donor carboxyfluoscein"
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/note= "optionally laballed with the acceptor
.6-carboxyrhodamine"
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100.0%; Pred. No. 1.7
:ive 0; Mismatches
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Gaps

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Length 25 Indels

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WPI; 1998-414127/35.
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(SAKA/) SAKAKI Y.
                                                                                                                         Homo sapiens.
                                                                                                                                       14-DEC-1998;
                                                                                                                                             15-DEC-1997;
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                                                                                                    08-SEP-1999
                                                                                                                                   24-JUN-1999
                                                                                                                                                         Sakaki Y;
                                                                                                                      Synthetic
                                                                                               AAX84259;
                                                                                     RESULT 138
  Ju J;
                                                                                        AAX84259/
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The present sequence is a telomerase Oliog-dT-Primer, which can be used in a novel method for detecting telomerase activity. The method comprises adding to a test sample a lst primer, that serves as telomerase substrate, and nucleoside triphosphate (dNTP) and incubating to allow primer extension by the telomerase (dNTP) and incubating the extension product, immobilising the amplification product (AP) on a solid phase and qualitative and/or quantitative arction of AP, where the substrate primer is preferably from the detection of AP, where the substrate primer is preferably from the retrovirus. The method can be used to diagnose tumours and screen retrovirus. The method can be used to diagnose tumours and screen compounds for effector activity. Immobilisation of AP provides a compounds that is reproducibly representative of telomerase activity, signal that is reproducibly representation and climinates the need for gel electrophoretic separation and provides high sensitivity. Radioactive labels are not required and provides high sensitivity. Radioactive labels are not required and the method can be automated for routine use. Specific detection is the method can be automated for routine use. Specific detection is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         achieved by proper choice of hybridisation conditions, without separation of the telomerase extension product. A specific signal is generated by 1-10 cell equivalents, but for tumour analysis 10-1000 ng of tissue is usually used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Measuring telomerase activity, useful for tumour diagnosis and compound screening - by extending substrate primer, followed by amplification and immobilising product for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Telomerase; substrate; primer; detection; 5'-region; retrovirus; long terminal repeat 2; LTR-2; diagnosis; tumour; screening; effector compound; PCR; amplification; Oligo-dT-Primer; ss.
treatment (e.g. by gene therapy) of Alzheimer's disease.
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89.5%; Pred. No. 1.5e+02;
                                                                                                   Score 18; DB 1; Le
Pred. No. 1.8e+02;
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                                                 Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 other;
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                                                                                                      Query Match 1.6%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 18; Conservative 0; Mismatches
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AAT69640 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                          RESULT 139
                                                                                                                                                                                                                                                                                                                                                                    AAT69640/
                                                                                                                                                                                                                                                                                                                                                                                         SXS
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                                                                                                                                                                                                                                                                                   The present sequence exxemplified the primer of the invention, and is used to sequence Incyte clone 1 (AAV42737). The primer of the invention is labelled with a set of at least 2 different fluorescent labels. The set comprises an energy-transfer fluorescent label with at least 1 each of a donor fluorophore and an acceptor fluorophore capable of energy transfer, and separated by a distance x, and a second similar fluorescent label in which the separation distance is y, x and y being sufficiently different for the two fluorescent labels to produce distinct fluorescent signals. Fluorescent labels are useful in multicomponent analyses, e.g. as probes for fluorescent in situ hybridisation or especially as primers for DNA sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein inhibiting apoptosis, useful in the diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                        Set of energy-transfer fluorescent labels with donor and acceptor at different separations - useful for DNA sequencing allows use of fewer analysing wavelengths or an increased throughput
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1.6%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                      Example 1; Page 14; 30pp; English
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Length 19;

17;

Matches

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19

RESULT 140

AAQ75744,

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE files ARQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 17.8; DB 1; Length 2 90.5%; Pred. No. 1.6e+02; ive 0; Mismatches 2; Indels
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les 19; Conserv
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aggregate; 1
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              Synthetic.
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Matches
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        Gaps
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     Indels
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 2; Mismatches
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Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
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Analysis followed

AAQ75752;

AA075752

à g

01-NOV-1994,

Analysis; gaggregate; Synthetic.

AAQ75744;

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Gaps

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Length 21;

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                 Reverse transcription primer used in cDNA analysis technique.
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90.5%; Pred. No. 1.6e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                         restriction enzyme; ss
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                                                AAQ75776 standard; DNA; 21
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                                                                                                                           (first entry)
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-018287/03
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                                                                                                                                                                                                                           aggregate;
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            RESULT 144
AAQ75776/c
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESSE) files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (D) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (C) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                           Length 21;
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                                                                                                                                                                                                                      1.6%; Score 17.8; DB 1; 90.5%; Pred. No. 1.6e+02;
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Best Local Similarity
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Analysis; Synthetic.

AAQ75771;

RESULT 143

AAQ75771,

Query Match

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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llarity 90.5%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 2;
                                                                        Score 17.8; DB 1;
Pred. No. 1.6e+02;
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                                   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
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                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ7547-07578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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Pred. No. 1.6e+02;
0; Mismatches 2;
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                                                                                                                                                                                                    Disclosure; Page 8; 11pp; Japanese.
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aggregate, restriction enzyme, ss.
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                      93JP-0112515.
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AAQ75764 standard; DNA; 21
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Best Local Similarity
Matches 19; Conserv
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followed by
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
  Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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Best Local Similarity 90.5'
Matches 19; Conservative
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AAQ75616/c
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                                                       Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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Reverse transcription primer used in cDNA analysis technique.
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90.5%; Pred. No. 1.6e+02;
tive 0; Mismatches 2; Indels
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les 19; Conservative
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                                                Analysis; gene
                                                                                                                                                                    JP06303997-A
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Gaps

0;

Indels

Length 21;

1.6%; Score 17.8; DB 1; 90.5%; Pred. No. 1.6e+02;

90.5%; Pred.

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                                                                                                 Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                  amplification of mRNA
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                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplifollowed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                      TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 6, 11pp; Japanese.
                                                                                                                   aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.5%;
                                                                                                                                                                                                                                93JP-0112515
                                                                                                                                                                                                                                                           93JP-0112515
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                                                                                                                                                                                                                                                                                                                WPI; 1995-018287/03.
                                                                                                                                                                                                                                                                                       (NITE ) NIPPON
                                                                                                                                                                                                                               16-APR-1993;
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93JP-0112515

(first entry)

93JP-0112515

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A method for the analysis of cDNA comprises (a) preparing an aggragate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs
                                                                                                                                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.8; DB 1; Length 21;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analysis of cDNA and gene expression - by ampl. followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                          Disclosure, Page 7; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGCAAAAAAAAAAAAA 1
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ilarity 90.5%;
Conservative 0
                                                                                 93JP-0112515.
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                                                                                                                                                                           WPI; 1995-018287/03
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                                                                                                                                                                                                                                                                                                                                                                                                                         rapidly and easily.
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hes 19; Conserv
               JP06303997-A.
                                                                             16-APR-1993;
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                                               01-NOV-1994.
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AAQ75648/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%; Score 17.8; DB 1;
90.5%; Pred. No. 1.6e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEGRAPH & TELEPHONE CORP.
   1080 TATTAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCAAAAAAAAAAAAAA
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                                                                                                                 AAQ75624 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ75664 standard; DNA; 21
                                                                                                                                                                                (first entry)
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Best Local Similarity 90.55
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-018287/03.
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                                                                                                                                                                                                                                             Analysis;
                                                                                                                                                                                                                                                                                              Synthetic
                                 21
                                                                                                                                                 AAQ75624;
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Gaps

0;

amplification of mRNA

us09904568-1.rng

BP.

standard; DNA; 24

27-SEP-1999

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AAZ00877;

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and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as th template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting onset of diabetes mellitus comprises detecting specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method using a mutation in the CD38 gene (involved in the production of cyclic ADP-ribose (CADPR)), to detect the onset of diabetes mellitus. The method is useful for detecting the onset of diabetes mellitus. The present sequence represents a PCR primer for human CD38, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; CD38; diabetes mellitus; detection; cyclic ADP-ribose; CADPR;
                                                                                                                                                     Length 21;
                                                                                                                                                                               Indels
                                                                                                                                                  Score 17.8; DB 1;
Pred. No. 1.6e+02;
                                                                                                                Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 2 A; 10 C; 2 G; 7 T; 0 other;
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Human CD38 exon 4 PCR primer SEQ ID NO:9.
                                                                                                                                                                                                       1080 TATTAAAAAAAAAAAA 1100
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l Similarity 90.5%;
19; Conservative
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                                                                                                                                                                                                                                                                                                        AAF32494 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the CD38 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BMLB-) BML KK.
(KANE/) KANETSUKA A.
(OKAM/) OKAMOTO H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-128255/14.
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
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                                                                                                                                               Query Match
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The invention relates to a mammalian PGI gene and protein, and a set of PGI biallelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Sally-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant procedure which would enable early-stage diagnosis. The PGI gene can be used for and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a prostate cancer associated gene and biallelic markers derived from it
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90.5%; Pred. No. 1.9e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                   Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CCR4 related protein 31 PCR primer 2.
                                                                                      PCR primer PGRT32 for PG1 coding sequence.
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97US-0996306.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                PSA; human; ss.
                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                Blumenfeld M,
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                      W09932644-A2
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Gaps

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1.6%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 1.6e+02; ive 0; Mismatches 2; Indels

995 AAGTCTGAGGCTGGAGAATGG 1015

Conservative

Local Similarity

Query Match

19;

Matches

21 AAGACGGAGGCTGGAGAATGG 1

g

RESULT 155 AAZ00877/c

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                                                                                                                                                                                                                                                                                                                                 Polypeptide-human CCR4 related protein 31 and polynucleotide for coding polypeptide, useful for treating e.g. cancer and HIV infection, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human CCR4 related protein 31, the polynucleotide encoding it and the use of the protein in treating e.g. cancer and HIV infection. The present sequence is that of a human CCR4 PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human fkbp protein 12.87 and encoding polynucleotide for treating malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; fkbp; 12.87; malignant tumour; haemopathy;
human immunodeficiency virus; HIV; infection; immunological disease;
inflammation; RT-PCR; primer; reverse transcription.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 17.8; DB 1; Length 24; 90.5%; Pred. No. 1.9e+02; live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 17 (Disclosure); 34pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human fkbp 12.87 specific RT-PCR primer #1.
                                                                                                                                                                                                                   CO LID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080 TATTAAAAAAAAAAAA 1100
                                                                                                                                                                                                               (SHAN-) SHANGHAI BORONG GENE DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATAAAAGAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                    polypeptide, useful for treat
prepared by DNA recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                    99CN-0124049
                                                                                                                                                                          99CN-0124049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-2000; 2000CN-0127372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS54833 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-714435/78.
                                                                                                                                                                                                                                                                                              WPI; 2001-489558/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                       Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xie Y;
                Homo sapiens
                                                                                                                                  22-NOV-1999;
                                                                                                                                                                          22-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                      CN1296960-A.
                                                                                             30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS54833;
                                                                                                                                                                                                                                                       Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 157
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                                                This invention relates to the DNA and protein sequences of a novel human Ekbp protein 12.87. The invention also comprises a method for producing the polypeptide by recombinant DNA technology. The polypeptide is useful in treating malignant tumours, haemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations. Also disclosed in the invention is an antagonist to the fkbp protein and a method for its use. The present sequence represents a reverse transcriptase (RT) PCR primer used to isolate the human fkbp 12.87 cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The method can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such a class 1/2 HLA comprises identifying all possible nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 17.8; DB 1; 90.5%; Pred. No. 1.9e+02;
Example 2; Page 17 (disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 5 A; 1 C; 3 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 TTCAGGTTTTGTTTTATGAGT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16s rRNA gene PCR primer #49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.6%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 5 A; 0 C; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2000; 2000WO-EP03636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99EP-0303215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC96082 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ulfendahl P, Wong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-679677/66.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of specific length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200065088-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 158
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hyperproliferative disease; ss.
                                                                                                                                       Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOUN ) MOUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1992;
02-FEB-1993;
07-JUN-1995;
                                                                   06-JUN-1995;
                                                                                             28-AUG-1992;
02-FEB-1993;
                                                                                   06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Homo sapiens
                                 US5756684-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                 26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5869622-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1999
                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAX04086;
                                                                                                                                                                                                                                                                                                                                                                               RESULT 161
                                                                                                                                                                                                                                                                                                                                                                                         AAX04086
à
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                                                                                                                                                                                                                                                                                                                                                                                         The oligonucleotides AAT99279-T99286 were used as competitor oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may be used to treat hyperproliferative diseases such as cancer.
                                                                                                                                  PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss; cancer; probe; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
                                                                                                                                                                                                                                                                                                                                        Assays for PUR protein ligands or modulators - using immobilised protein or fragments, to treat hyper-proliferative diseases, e.g. cancer
                                                                                                                POLYA, a competitor oligonucleotide for binding human PUR-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 17.6; DB 1; Length 24; 83.3%; Pred. No. 2e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of the oligonucleotide POLYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1077 AACTATTAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAAAAAAAAAAAAAAAAAA 24
    1077 AACTATTAAAAAAAAAAA 1097
                                                                                                                                                                                                                                                                                    (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                          Examples; Column 33; 64pp; English.
                      Н
                      ATCTCTTAAAAAAAAAAAAA
                                                                BP
                                                                                                                                                                                                                                                  92US-0938189.
93US-0014943.
95US-0486421.
                                                                                                                                                                                                                                          95US-0470911
                                                                                                                                                                                                                          95US-0486421
                                                               AAT99286 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                       Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV31743 standard; DNA;
                                                                                                                                                                                                                                                                                                                      WPI; 1997-488859/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                      Bergemann AD,
                                                                                                                                                                                                                                         06-JUN-1995;
28-AUG-1992;
02-FEB-1993;
                                                                                                                                                            Synthetic.
Homo sapiens
                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                 15-APR-1998
                                                                                                                                                                                     US5672479-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1998
                                                                                                                                                                                                        30-SEP-1997
                                                                                                                                                                                                                                                                    07-JUN-1995
                                                                                 AAT99286;
                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV31743;
                                               159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 160
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This is the nucleotide sequence of an oligonucleotide used as a competitor with the PUR element in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; ss.
                                                                                                                                                                                                                                                                                      - that inhibit PUR protein binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide POLYA used in PUR cloning and sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 17.6; DB 1;
83.3%; Pred. No. 2e+02;
rative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Example 7.1.1; Column 33; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1077 AACTATTAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ААААААААААААААААААААА
                                                                                                                                    (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                            PUR protein and its fragments
PUR element or other proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0470911,
92US-0938189,
93US-0014943,
95US-0486809,
                                                                 92US-0938189.
95US-0470911.
                                          95US-0470911.
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                                                                                                                                                                                       EW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-1999 (first entry)
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Past Local Similarity 83.5.7
70: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson EM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method (M1) for inserting a nucleic acid (M1) into a circular vector (V1) comprising joining ends of N1 and V1 under a first nucleic acid concentration, melting hybridized cohesive circularization ends, and reannealing the ends at a second concentration. The methods are useful for the cloning small amounts of nucleic acids and forming genomic libraries of complex populations of DNA or CDNA. The methods allow the cloning of minute amounts of uncleic acids efficiently and avoids the size selection problems of prior art systems. Larger nucleic acid fragments are just as easily cloned, allowing highly
                                                                                                                              The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR spec. The present sequence represents an oligomucleotide used in the cloning and sequencing of the PUR protein and its sequence element PUR repeat, in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inserting a nucleic acid into a circular vector comprising joining their ends, melting, and reannealing ends at two different concentrations, useful for cloning small amounts of nucleic acids and forming genomic libraries
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                     Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                       ·
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                                                                                                                                                                                                                                                                                                                                                                           ch 1.6%; Score 17.6; DB 1; Length 24; 1 Similarity 83.3%; Pred. No. 2e+02; 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                      Seguence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBluescriptSK+ phagemid primer SEQ ID NO: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1077 AACTATTAAAAAAAAAAAAA 1100
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                                                                                                 Example; Column 33; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; cloning; ligation; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA40353 standard; DNA; 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-442381/38.
WPI; 1999-152881/13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Romantchikov Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200036088-A1
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                                                                                                                                                                                                                                                                                                invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 162
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inserting a nucleic acid into a circular vector comprising joining their ends, melting, and reannealing ends at two different concentrations, useful for cloning small amounts of nucleic acids and forming genomic libraries -
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representative libraries to be made. Vector to vector ligation is avoided using the methods, AAA40351-A40366 represents primers used illustrate the method of the invention.
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                                                                                                                                                             1.6%; Score 17.6; DB 1; Length 24; 33.3%; Pred. No. 2e+02;
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                                                                                                         Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBluescriptSK+ phagemid primer SEQ ID NO: 9.
                                                                                                                                                                                                                   0; Mismatches
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0; Mismatches
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                                                                                                                                                                                      83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer; cloning; ligation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA40359 standard; RNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-2000 (first entry)
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROMA/) ROMANTCHIKOV Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442381/38.
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Matches 20; Conserv
                                                                                                                                                                                         Local Similarity
tes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Romantchikov Y;
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                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 163
                                                                                                                                                                                                                      Matches
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Vaccine, cytostatic, virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinating against tumors, infectious diseases, allergies and asthmaushing immunostimulatory Py-rich and TG nucleic acids -
               Immunostimulatory nucleic acid #872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 101; Page 57; 338pp; English.
                                                                                                                                                                                                                                                                                                 99US-0156113.
                                                                                                                                                                                                                                                          25-SEP-2000; 2000WO-US26383.
                                                                                                                                                                                                                                                                                                                                                                     (IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                                 27-SEP-1999; 99US-0156135.
                                                                                                                                                                                                                                                                                                                                                                                                                             Krieg AM, Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-273485/28
                                                                                                                                                                                  WO200122972-A2.
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27-SEP-1999;
                                                                                                                                                                                                                       05-APR-2001
                                                                                                                                               Synthetic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an nucleic acid. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) for thymidine (T) rich. The method is used to vaccinate subjects and/or orthowyxoviridae), bacterial antigens (e.g. herpesviridae, retroviridae and/or orthowyxoviridae), bacterial antigens (e.g. toxoplasma, staphylococcus), fungal antigens and/or present antigens and/or preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a limmune cells.
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                                                                                                                                                                                    Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids
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83.3%; Pred. No. 2e+02;
iive 0; Mismatches
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                                                                                                                                                     Immunostimulatory nucleic acid #420.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vollmer J;
                                          AAF99304 standard; DNA; 24 BP.
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23-AUG-2000; 2000US-0227436.
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(COLE-) COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2000; 2000WO-US26383
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                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-273485/28
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                                                                                                                                                                                                                                                                                                                    WO200122972-A2.
                                                                                                                12-JUN-2001
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                                                                                                                                                                                                                                                                                   Synthetic
                                                                             AAF99304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
       RESULT 164
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                           AAF99304/
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Vollmer J;

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, and/or crampylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parastic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a immune deficiency. The present sequence can also be used to redirect a rock the present sequence may have a phosphorothicate backbone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 17.6; DB 1; Length 24; 83.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
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Best Local Similarity
Matches 20; Conserv
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AAF99756 standard; DNA; 24 BP

RESULT 165

g ð

(first entry)

12-JUN-2001

AAF99756;

AAF99756/c ID AAF9 XX AC AAF9 XX DT 12-J

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                  Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 17.6; DB 1; Length 24; 83.3%; Pred. No. 2e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 14833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1077 AACTATTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 АААААААААААААААААААА 24
                                                                                                                                                                                                                                                                                                                                                Claim 101; Page 57; 338pp; English
                                                                                                                                                                                                                                     Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                       25-SEP-1999; 99US-0156113.
27-SEP-1999; 99US-0156135.
23-AUG-2000; 2000US-0227436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-183319P.
2000US-189862P.
                                                                                            25-SEP-2000; 2000WO-US26383.
                                                                                                                                                                                        (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV14842 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                       (COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmacogenomic marker;
                                                                                                                                                                                                                                     Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate
                            WO200122972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2002
                                                           05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001
                                                                                                                                                                                                                                     Krieg AM,
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV14842,
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                              (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17.6; DB 1; Length 24;
Pred. No. 2e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anglogenesis inhibitory oligonucleotide #433.
                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1077 AACTATTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                            Claim 1; Page 2483; 11750pp; English
                                                                                                                                 Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 1.6%;
1 Similarity 83.3%;
20; Conservative
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-255281P.
13-DEC-2000; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS77949 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                              cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2002
                                                                                                                               Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS77949;
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antiangiogenic nucleic acid molecule to the subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                     one
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                                 {\tt E} \overset{\mathsf{M}}{\mathsf{M}} \overset{\mathsf{M}} \overset{\mathsf{M}}{\mathsf{M}} \overset{\mathsf{M}}{\mathsf{M}} \overset{\mathsf{M}}{\mathsf{M}} \overset{\mathsf{M}}{\mathsf{M}} \overset{\mathsf{M}}{\mathsf{M}} 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering the a subject having a condition characterised by unwanted anglogenesis. The method is useful for inhibiting angiogenesis associated with solid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, mecular degeneration, corneal graft rejection, neovascular glaucoma mecular degeneration, conneal graft rejection, neovascular glaucoma methologis, only solid sia, rubeosis, older webber Syndrome, mycardial angiogenesis plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions.
                                                                                                                                                                                                                                                                    Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 17.6; DB 1;
13.3%; Pred. No. 2e+02;
.ve 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 0 A; 0 C; 0 G; 24 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       joints, angiofibroma, wound granulation, atherosclerosis, scleroderma and hypertro
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 27; 276pp; English.
(COLE-) COLEY PHARM GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COLE-) COLEY PHARM GROUP INC.
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les 20; Conserv
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                                                                                              Bratzler RL;
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule.

Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis.

The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthitis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, oller-Webber Syndrome, myocardial angiofibroma, wound granulation, intestinal adhesions, cionis, atherosclerosis, scleroderma and hypertrophic scars. The present consists of the contestion intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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Also included is a kit comprising a first container housing the
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to inhibiting angiogenesis in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 17.6; DB 1
83.3%; Pred. No. 2e+02;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitory oligonucleotide #962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AAAAAAAAAAAAAAAAAAAA
Claim 2; Page 36; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 36; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-2001; 2001WO-US48458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-2000; 2000US-255534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS78478 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-566690/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200253141-A2
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       antiangiogenic nucleic acids, and instructions for administering them to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the detection of multiple components in a medium, comprising combining the medium with at least two sensitiser reagents, and at least one reactive reagent activated by a product generated by the sensitiser reagents when activated; and differentially activating the sensitiser reagents. The combination of sensitiser reagents and reactive reagent(s) allows differential detection of the components. Methods of the invention may be used for the detection of ligands, receptors and polynucleotides, and also for the detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of multiple analytes, e.g. ligands, receptors, polynucleotides and pollutants, involves adding a combination of sensitiser reagents and reactive reagent actuatable by a product of the
                        a subject having a condition, characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retroolental fibroplasia, rubeosis, Osler Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telanglectasia, haemophiliac loints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/label= OTHER
/note= "modified by PO2OCH2CH2CH2SSCH2CH2CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 17.6; DB 1; Length 24; 83.3%; Pred. No. 2e+02; 1ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Keczer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A24 oligonucleotide for the creation of Pc-A24.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kurn N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA98840 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cromer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-164078/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA98840;
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AC ABA9

AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism detection; sequence detection; mutation detection; A24; probe; non-dissociative termolecular complex; dopTAR sensitiser particle; single nucleotide polymorphism; SNP; ss.
e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated biphenyls, phosphate esters, thiophosphates, carbamates and polyhalogenated sulfenamides) and pollutants. Methods of the invention allow the detection of multiple analytes in a single test medium. An application of the methods of the present invention would be in the field of clinical diagnostics. The current sequence represents A24 oligonucleotide for the creation of oligonucleotide coated
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A24 oligonucleotide used to create dopTAR chemiluminescer particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting presence of polynucleotide, differences between polynucleotide sequences, useful for detecting single nucleotide polymorphism and alleles of polynucleotide sequence involves use of
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                                                                                                                                                                                                 Length 24;
                                                                                                                                                                                                                                    Indels
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/note= "A is covalently linked to a
PO2OCH2CH2CH2SSCH2CH2OH moiety"
                                                                                                                                                                                                                                    4;
                                                                                                                                                                                               1.6%; Score 17.6; DB 1;
83.3%; Pred. No. 2e+02;
                                                                                                                                                              Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                          phthalocyanine sensitiser particles (Pc-A24)
                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                    1077 AACTATTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                        83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                               AAS17869 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             three competitive probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-097664/13.
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200190399-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
modified base
                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS17869;
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                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                           RESULT 172
                                                                                                                                                                                                                                  Matches
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the polynucleotide sequence with the first and second probes or the polynucleotide sequence with the first and third probes. The oligonucleotide probes have labels non-covalently bound to allow for their detection upon binding. The method of the invention is useful for detecting the presence of a single nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method can be used for the direct detection of nucleic acid in very small quantities without amplification. In addition, the method may be carried out with amplification of the target probe A24 used to create doppha chimiluminescer sensitiser particles in the method of the invention. Binding the nucleic acid to a suspendable polynucleotide target from the bulk solution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.6%; Score 17.6; DB 1; Length 24; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
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1 AAAAAAAAAAAAAAAAAAAAA 24 RNA-PCR procedure primer poly(dT)24. BP 639/c ABK15639 standard; DNA; 24 (first entry) 08-MAY-2002 ABK15639; RESULT 173 ABK15639, THE STATE OF THE S

RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy; mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense; high throughput screening; D-RNAi; DNA-RNA interference; RdRp; RNA dependent RNA polymerase; posttranscriptional gene silencing.

Synthetic.

WO200210374-A2.

07-FEB-2002.

02-AUG-2001; 2001WO-US24412.

02-AUG-2000; 2000US-222479P.

Chuong C, Widelitz RB; Lin S,

(UYSC-) UNIV SOUTHERN CALIFORNIA,

WPI; 2002-188740/24

The invention relates to generating mRNA-cDNA hybrids, comprising

(a) providing a solution containing a nucleic acid template, one or more primers complementary to the sense conformation of the nucleic acid template, and one or more promoter-linked primers complementary to the antisense conformation of the nucleic acid template, and with an RNA promoter, (b) treating the nucleic acid template with the one of more primers to synthesise a first cDNA strand, (c) treating the first cDNA strand with one or more promoter-linked primers to synthesise a promoter-linked double-stranded nucleic acid, (d) treating the promoter-linked double-stranded nucleic acid, (d) treating the promoter-linked clouble-stranded nucleic acid, (e) treating the mRNA fragments and (e) treating the mRNA fragments with one or more primers to synthesise treating or preventing microbe related genes, comprises thermocycling steps of promoter-linked double-stranded cDNA or RNA synthesis Generating mRNA-cDNA hybrids for suppressing cancer-related genes, Example 5; Page 26; 53pp; English.

mRNA-cDNA hybrids by reverse transcription of the amplified mRNA fragments. The method is useful for preparing high amounts of pure and fragments. The method is useful for preparing high amounts of pure and specific mRNA-cDNA hybrids for transducing biological effects of interest in vitro as well as in vivo, for inhibiting gene function in prokaryotes and eukaryotes in vivo, for inhibiting gene function in carcarded genes, in tracting or preventing microbe related genes, in studying candidate molecular pathways with systematic knock out of involved molecules, in high throughput screening of gene functions in physiological conditions. The mRNA-cDNA hybrids may be used to in physiological conditions. The mRNA-cDNA hybrids may be used to screen for special gene functions, for manipulating gene expression in vitro, and for designing therapy for genetic diseases in vivo. The cDNA part of a D-RNAi (DNA-RNA interference) can be modified by nucleotide ransfected probe activities. The RdRA (RNA dependent RNA polymerase) errorparation to increase the stability and effectiveness of transfected probe activities. The RdRA (RNA dependent RNA polymerase) compared to ds-RNA duplexes. The RdRA dependent RNA provides further antisense gene knockout activity in addition to the posttranscriptional gene silencing (PTGS) mechanisms of the sense-RNA template, resulting in multiple specific gene interference effects with one probe. The present sequence is a poly (dT) PCR primer used in the series of the series. first strand cDNA in the method of the invention

1.6%; Score 17.6; DB 1; Length 24; 13.3%; Pred. No. 2e+02; ve 0; Mismatches 4; Indels Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other; Query Match 1.6%; Best Local Similarity 83.3%;

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Gaps

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1077 AACTATTAAAAAAAAAAAAA 1100 24 АААААААААААААААААА 1 à 셤

20; Conservative

Matches

ABL39405 standard; DNA; 24 16-APR-2002 (first entry) ABL39405; RESULT 174 ABL39405/

ВР

Immunostimulatory nucleic acid SEQ ID NO: 841.

Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.

Synthetic.

/note= "phosphorothioate backbone" Location/Qualifiers 1..24 /*tag= a /mod_base= OTHER Key modified_base

WO200197843-A2

27-DEC-2001

22-JUN-2001; 2001WO-US20154. 22-JUN-2000; 2000US-213346P.

(IOWA) UNIV IOWA RES FOUND.

Hartmann G; Weiner G,

WPI; 2002-154611/20.

Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of

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                                                                                                                                                        The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression
                                                                                                                                                                                                                                                      of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, cervical cancer, eye cancer, kidney cancer, larynx cancer, levkaemia, liver cancer, ind cancer, hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, proceste cancer, independence, ovarian cancer, stomach cancer, resticular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in
of
surface antigens and antibodies to a subject having or at risk
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Pred. No. 2e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the invention.
                                                                                                 Disclosure; Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ААААААААААААААААААААА 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ACA58802/
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Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of prevention or treatment of gastric ulcer comprising administering a nucleic acid to a subject in need for treatment of gastric ulcer. A nucleic acid sample comprising oligonucleotide 2006 was administered to a mouse model by an oral route or a vehicle control. Colonisation of mice by Heliobacter pylori was assessed at time points from 1 day to 1 month after treatment. The ability of the nucleic acid to reduce H. pylori colonisation was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prevention or treatment of gastric ulcer involves administering nucleic
Gastric ulcer treatment immunostimulatory nucleic acid #148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2001; 2001US-0920313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-222248P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersen DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-370798/35.
                                                                                                          Heliobacter pylori
                                                                                                                                                                                                                                           US2002198165-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-2000;
                                                                                                                                                                                                                                                                                                                 26-DEC-2002.
                                                                                                                                                                         Synthetic.
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assessed. The method is useful for preventing or treating a gastric ulcer on a subject e.g. human or non-human vertebrate animal including dog, cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig, rabbit, turkey, chicken, primate, rat and mouse. The method effectively treats or prevents gastric ulcers. The present sequence represents an immunostimulatory nucleic acid for the treatment of gastric ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulation; immune response; natural killer cell; interferon; type 1 interferon; IFN; cancer; infectious disease; allergic disorder; immune related disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulatory nucleic acid, useful for preparing a composition
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally phosphorothioate backbone"
                                                                                                                                                            Length 24;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                4;
                                                                                                                                                            1.6%; Score 17.6; DB 1;
13.3%; Pred. No. 2e+02;
.ve 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory oligonucleotide SEQ ID NO:53.
                                                                                                                           Seguence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                                                                1077 AACTATTAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                  AAAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating an allergic condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLEY PHARM GROUP INC COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                              ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-2002; 2002WO-US2646B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-313273P.
2002US-393952P.
                                                                                                                                                                                                                                                                                                                                                      ABZ80181 standard; DNA; 24
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-268241/26.
                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003015711-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2001;
03-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       ABZ80181;
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                                                                                                                                                               Query Match
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Matches
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us09904568-1.rng

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Gaps

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can be used in gene therapy. (I) can be used for preparing a composition for treating a variety of immune related disorders such as cancer, infectious diseases and allergic disorders. (I) also stimulates the activation of natural killer cells and the production of type 1 interferon (IFN). The present sequence represents an immunostimulatory oligonucleotide, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel method of immobilising oligonucleotides to a solid support by incubating in the presence of a salt or cationic detergent e.g. Nacl (50-250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3 carbodismide hydrochloride (ECD). The oligonucleotides can be capture probes for detection of specific nucleic acids by hybridisation or can be primers for template-dependent extension from the immobilised primers on nucleic acid from a target organism. The method can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immobilisation; solid support; salt; cationic detergent; capture probe; hybridisation; primer; template-dependent extension; target organism; sequencing; genetic polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on nucleic acid from a target organism. ALE MINIOUS acid from a seays, sequencing and analysis of genetic polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immobilising synthetic nucleic acid on solid support - by incubation in presence of salt or cationic detergent, for use in hybridisation assays, sequencing and analysis of polymorphism
                                                                                                                                                      1.6%; Score 17.6; DB 1; Length 24;
83.3%; Pred. No. 2e+02;
ive 0; Mismatches 4; Indels
                                                                                                                    Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
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/note= "biotinylated"
                                                                                                                                                                                                                                                         AAAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                        83.3%;
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93US-0162397
                                                                                                                                                                                                                                                                                                                                         AAQ95960 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                          Conservative
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                                                                                                                                                                      Local Similarity
les 20; Conserv
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misc_feature
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                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                         RESULT 177
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1.6%; Score 17.6; DB 1; Length 25;

Query Match

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                                                                                                                                                                                                                 Nck associated protein 1; Napl; human; apoptosis; Alzheimer's disease;
therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein 1 (Napl) of the invention. Napl inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease.
                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein inhibiting apoptosis, useful in the diagnosis and treatment
                 0;
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                                                                                                                                                                                        PCR primer for human Nck associated protein 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
   Pred. No. 2.1e+02;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 17.6; DB 1;
83.3%; Pred. No. 2.1e+02;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 other;
                                   1077 AACTATTAAAAAAAAAAAAA 1100
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                                                          25 AAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16s rRNA gene PCR primer #168.
                                                                                                                                                                                                                                                                                                                                                                                 HAKKO KOGYO KK.
   83.38;
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                                                                                                                       23
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                                                                                                                                                                  (first entry)
Similarity 83.3
20; Conservative
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Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                     DNA;
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ID AAC96201 Btandard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-395181/33.
                                                                                                                    AAX84260 standard;
                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAK
(SAKA/) SAKAKI Y.
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                   W09931239-A1
                                                                                                                                                                                                                                                                                                                                  14-DEC-1998;
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              20;
                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                            AAX84260;
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 Best Local
Matches 2
                                                                                             RESULT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                       The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 17.6; DB 1; Length 25; 83.3%; Pred. No. 2.1e+02; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAACTATTAAAAAAAAAAAA 1098
                                                                                                                                        (AMSH ) AMERSHAM PHARMACIA BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMSH ) AMERSHAM PHARMACIA BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGACTGAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                  Claim 14; Page 47; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA HLA-C gene PCR primer #63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                       20-APR-2000; 2000WO-EP03636.
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                                                                                                                 99EP-0303215
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Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                   Wong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong K;
                                                                                                                                                                                          WPI; 2000-679677/66.
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                                    WO200065088-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1999;
             Homo sapiens
                                                                                                                                                                  Ulfendahl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                26-APR-1999;
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                                                              02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                       particular.
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                             as
                                                                                                                                    The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such a class 1/2 HLA comprises identifying all possible nucleotide sequences of specific length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; probe; target nucleic acid; enzymatic amplification;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                           Length 25
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                                                                                                                                                                                                                                                                                                                           1.6%; Score 17.6; DB 1;
83.3%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                        Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      1073 AAGCAACTATTAAAAAAAAAA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weller DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Column 17; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCGGCTACTAAAAAAAAAAAA
                                                                                                Claim 14; Page 58; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rapid detection; probe; tisolation; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-364413/31.
                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA39306;
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do not interfere with amplification of target molecule. AAA39316 to AAA39316, represent oligonucleotides used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Attaching capture probes to solid phases through non-nucleic spacers, producing arrays for detecting interactions of proteins with other
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to screen for interactions between proteins and compounds (e.g. other proteins, ligands or mucleic acids), particularly to identify potential therapeutic agents, enzyme substrates or unknown proteins that interact with drugs, but also for diagnosis (detecting disease-associated proteins) and for quantifying target molecules in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents a capture probe specific for a c-myc
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1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c-myc fusion, non-nucleoside spacer; capture probe; nucleic acid-protein fusion; ribosome display particle;
                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                       Capture probe CP125 specific for c-myc fusion targets.
                                                                                                              Score 17.6; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 other;
                                                                             Sequence 25 BP; 0 A; 0 C; 0 G; 25 U; 0 other;
                                                                                                                                                                                           1077 AACTATTAAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compounds, e.g. for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Page 29; 57pp; English.
                                                                                                                                                                                                                               25 AAAAAAAAAAAAAAAAAAAA
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                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                          AAZ30267 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013048/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHYL-) PHYLOS INC.
                                         present invention.
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The invention relates to a method of preparing a controlled pore glass-polytetrafluoroethylene (PTFE) resin chromatography membrane, comprising controlled pore glass and an aqueous dispersion of PTFE to form a paste-like mass, heating the paste-like mass at 50-70 plus oC, calendering to form a foldable sheet, and sintering the sheet to produce a rigid, porous sheet. The method prepares a controlled pore glass-PTFE resin chromatography membrane for use in various biotechnical procedures. The membrane is useful in place of controlled pore glass as a support for the synthesis, isolation, and purification of nucleic acids and for the tisolation and purification of proteins. The method produces a membrane that may be used in lieu of controlled pore glass. The present sequence represents an oligonucleotide prepared on the membrane in an example which demonstrates the method of the invention.
                                                                                                                                                                                                                                        Glass-synthetic resin membrane; pore glass-polytetrafluoroethylene resin; chromatography membrane; PTFE; ss.
                                                                                                                                                                                                           Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of controlled pore glass-polytetrafluoroethylene resin chromatography membrane by heating, calendering and sintering mixture of controlled pore glass and aqueous dispersion of polytetrafluoroethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 17.6; DB 1; Length 25; 83.3%; Pred. No. 2.1e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 other;
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1077 AACTATTAAAAAAAAAAAAAA 1100
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                           25 AAAAAAAAAAAAAAAAAAA
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                                                                                                 986/c
ABK49986 standard; DNA; 25
                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPGC-) CPG INC
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                                                                                                                                                                            15-JUL-2002
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                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                            ABK49986;
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AAQ75556/c
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Matches
                                                                             RESULT 183
                                                                                              ABK49986/
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A method for the analysis of cDNA comprises (a) preparing an angaregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 17.4; DB 1; Length 1 94.7%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                       Disclosure, Page 5; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1082 TTAAAAAAAAAAAAA 1100
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                                                                Analysis of followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                    Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplification of mRNA
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                                                                        transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
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1.6%; Score 17.4; DB 1;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by ampl followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;
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AAQ75548 standard; DNA; 19 BP.
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   04-AUG-1995
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                                                                                                                                            Analysis;
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Gaps

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Length 19;

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A method for the analysis of CDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENBSER files ARQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                          reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                      Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                        Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5; 11pp; Japanese.
                                                                                                                          Jene expression; reverse
restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03

93JP-0112515 93JP-0112515

16-APR-1993; 16-APR-1993;

01-NOV-1994

18;

Matches

à d 04-AUG-1995

AAQ75598

RESULT 187

aggregate; Synthetic

Analysis;

01-NOV-1994

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primer she for second carbon and a plural type of labelled reverse transcription primer she from the mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                                                                  cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 1;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
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                                                                                                                                                                               (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 5; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
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                                  JP06303997-A.
                                                                                                         16-APR-1993;
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of
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aggregate;
 Synthetic.
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                      gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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 Indels
1;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5; 11pp; Japanese.
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                                   1082 TTAAAAAAAAAAAAAA 1100
0;
                                                                     20 TTGAAAAAAAAAAAA 2
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                                                                                                                                                              AAQ75598 standard; DNA; 20
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Conservative
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Les 18; Conserv
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Query Match

Best Loca Matches

AAQ75595,

RESULT 188 AAQ75595/c

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Gaps

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and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction seperate lanes, (c) electrophoresing the digested aggregate of cDNAs in enzyme and; (c) electrophoresing the used to analyse gene expression
                                                                                                                                                                                                                          Gaps
aggregate of double-stranded cDNAs by using an aggregate of mRNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                   Score 17.4; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysis of cDNA and gene expression - by ampl.
followed by digestion with restriction enzymes
                                                                                                                                               Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
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                                                                                                                                                                                                                                               1082 TTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction enzyme; ss.
                                                                                                                                                                                                                                                                                   19 TCAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                 rapidly and easily
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                                                                                                                                                                                                                                                                                                                                  RESULT 190
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate (c DNAs in separate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like growth factor binding protein-5; IGFBP-5; human;
antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
breast cancer; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                           expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                   Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.4; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 5; llpp; Japanese.
                                                                                                                           restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1082 TTAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense IGFBP-5 inhibitor #13.
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           BP.
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          AAQ75564 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rapidly and easily.
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                                                                                                           Analysis; gene
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                                                           04-AUG-1995
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                                                                                                                          aggregate;
                                                                                                                                                  Synthetic.
                                  AAQ75564;
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AAQ75564
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Gaps

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1; Indels

Length 20;

Score 17.4; DB 1; Pred. No. 1.8e+02;

1.6%;

0; Mismatches

1082 TTAAAAAAAAAAAAA 1100

à

Conservative

Local Similarity

Query Match

18;

Best Loca Matches TCAAAAAAAAAAAAA 1

19

by amplification of mRNA

expression -

gene

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gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                    Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                    aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                           (first entry)
                   (UYBR-) UNIV BRII
(MIYA/) MIYAKE H.
         19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                              Synthetic
                                  Gleave M;
                                                                                                                                                                                                                                                                                                              Analysis;
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                                                                                                                                                                                                                                                           RESULT 193
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENBSEQ files AAQ75547_Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                   digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                       Disclosure; Page 8; 11pp; Japanese.
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Matches 18; Conservative
                                                                                                                        Analysis of cDNA and followed by digestion
                                                                  WPI; 1995-018287/03.
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aggregate; rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an antisense oligomucleotide targeted against human insulin-like growth factor binding protein-5 (IGFBP-5). The invention relates to a composition for treatment of hormone-regulated cancer, comprising an antisense oligomucleotide (such as this sequence) which inhibits expression of IGFBP-5 by hormone-regulated tumour cells. The compositions is useful for delaying progression of hormone-regulated androgen-independent state, by treating hormone sensitive tumour cells with the antisense sequence which inhibits expression of IGFBP-5 by the tumour cells. The composition can also be used for treating a hormone-responsive cancer in an individual, and administering the composition to the individual after initiation of hormone-withdrawal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                             Composition for treating hormone-regulated cancer, e.g. breast and profetatic tumoures, comprising an antisense oligomucleoride that inhibits expression of ingulin like growth factor binding protein-5 by hormone-regulated tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          induce apoptotic cell death of hormone-responsive tumour cells, and therefore delaying the progression of hormone-responsive cancer cells to anhormone-independent state in the individual. It can also be used for inhibiting or delaying metastatic boney progression of an IGF-1 sensitive tumour in a mammal, by administering the composition to inhibit the expression of IGFBP-5 by the hormone-responsive cancer cells, and therefore inhibiting or delaying metastatic boney
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Pred. No. 1.8e+02;
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                                                                                                            BRITISH COLUMBIA.
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Matches 18; Conservative 0
19-JUL-2000; 2000WO-CA00853.
                                                      99US-0144495.
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Length 21;

1.6%; Score 17.4; DB 1; Length 2: 94.7%; Pred. No. 1.98+02; No. 1.98+02; I Indels

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                             gene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
                                                               Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 8; 11pp; Japanese
                                                                                                                                                                                                                                    93JP-0112515.
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Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

rapidly and easily.

Query Match Best Local S: Matches 18,

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESE) files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                 of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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les 18; Conserv
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                                                     Synthetic.
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                           expression; reverse transcription; primer; cDNA;
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            Length 21;
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                             Indels
          Score 17.4; DB 1;
Pred. No. 1.9e+02;
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                                           0; Mismatches
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                                                                            1082 TTAAAAAAAAAAAAA 1100
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ilarity 94.7%;
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AAQ75772 standard; DNA; 21
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JP06303997-A.

aggregate;

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                            A method for the analysis of CDNA comprises (a) preparing an aggregate of double-stranded CDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded CDNAs with restriction enzyme and; (c) alectrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                 1.6%; Score 17.4; DB 1; Length 21; 94.7%; Pred. No. 1.9e+02; ive 0; Mismatches 1; Indels
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1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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   8; llpp; Japanese.
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Disclosure;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ7547-Q758) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of
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                                                                                                                               ene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
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                          AAQ75763 standard; DNA; 21
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aggregate; rest
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                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                    of cDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of CDNA and gene expression - by amplification of mRNA by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                    Length 21;
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                                                                                                                                                                                                                                                                               Score 17.4; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                          Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
                                                           (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                Disclosure; Page 9; 11pp; Japanese
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                     93JP-0112515
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                                                                                                                                                                                                                                                                                                   18; Conservative
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                    16-APR-1993;
                                         16-APR-1993;
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oue prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                           1; Indels
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                                                                                                                                                             Score 17.4; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                            1082 TTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggregate; restriction enzyme; ss.
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AAQ75630 Btandard; DNA; 21
                                                                                                                 Sequence 21 BP; 1 A; 3 C;
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                                                                                                                                                                                                       Conservative
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Best Local Similarity
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followed by
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ID AAQ7
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the analysis of cDNA comprises (a) preparing an double-stranded cDNAs by using an aggregate of mRNAs

cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes

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and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lames. The method can be used to analyse gene expression
                                                                                                                                                                                                                                  Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
                                                                               Disclosure; Page 6; 11pp; Japanese
                    WPI; 1995-018287/03.
                                                                                                                                                                                                            rapidly and easily
                                                                                                                       aggregate of
                                                                                                          A method for
                                             Analysis (followed)
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AAQ75638/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                      cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
                                                                         Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                             Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 1;
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l Similarity 94.7%;
18; Conservative
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                        (first entry)
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followed by
                        04-AUG-1995
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                                       Gaps
                                     0;
                                                                                                                                                                                                                                                                                              Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                  Reverse transcription primer used in cDNA analysis technique.
 ch 1.6%; Score 17.4; DB 1; Length 21; l Similarity 94.7%; Pred. No. 1.96+02; 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6; 11pp; Japanese.
                                                             1082 TTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                 restriction enzyme; ss
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                                                                                                                                                                     AAQ75638 standard; DNA;
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Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                 aggregate;
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gene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

93JP-0112515 93JP-0112515

16-APR-1993;

JP06303997-A.

aggregate; Analysis;

Synthetic

01-NOV-1994

Reverse transcription primer used in cDNA analysis technique.

RESULT 206

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75788) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                 by amplification of mRNA enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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Pred. No. 1.9e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                 cDNA and gene expression - digestion with restriction
                                                                                                                                                                                                                                                                               gene expression
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             aggregate; restriction enzyme;
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AAQ75626 standard; DNA; 21
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                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSESP files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - by amplification of mRNA
on enzymes
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1.6%; Score 17.4; DB 1; Length 21; 94.7%; Pred. No. 1.9e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 17.4; DB 1; Length 21; 94.7%; Pred. No. 1.96+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of cDNA and gene expression - followed by digestion with restriction
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AAQ75625 standard; DNA; 21
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                                    Conservative
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Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-018287/03.
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Best Local Simi
Matches 18;
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Disclosure; Page 6; 11pp; Japanese.

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AAQ75625

AAQ75625/ ID AAQ7 XX AC AAQ7 XX DT 04-A' XX XX XX XX XX XX XX XX XX Anal:

RESULT 207

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Gaps

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Indels

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Gaps

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Indels

Length 21;

DB 1;

Score 17.4; DB 1; Pred. No. 1.9e+02;

1.6%;

0; Mismatches

BP.

(first entry)

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQTS547-QPS) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75247-07538) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression; reverse transcription; primer; cDNA;
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1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggregate; restriction enzyme; ss.
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AAQ75627 standard; DNA; 21
                                                                                                                                                                                                                                                              18; Conservative
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVIS4T-QTS7S) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoreasing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                            expression; reverse transcription; primer; cDNA;
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                                                                    Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 6; 11pp; Japanesė.
                                                                                                        restriction enzyme; ss.
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AAQ75644 standard; DNA; 21
                                              (first entry)
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Best Local Similarity
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                                                                                              gene
                                                                                                                                                     JP06303997-A.
                                                                                                                                                                                                    16-APR-1993;
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                                                                                                        aggregate;
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                                                                                                                               Synthetic.
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Matches
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Polymorphism, human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss. Homo sapiens

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          22-DEC-1999;
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                                                                                         Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for identifying an inhibitor of potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic forms of the gene for an each somethod can be used in the diagnosis, prevention and treatment of LOH disorders, contagned at the casions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZSBA12-ZSBA25
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                                                                                                                                                                                                                                                                                                       Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease
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gene therapy; PCR primer; ss.
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Figure 7; 605pp; English.
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94.7%;
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                                                                                                                                                                                 (VARI-) VARIAGENICS INC.
                                                                                                                                                                                                                            Ledley FD,
                                                                                                                                                                                                                                                                     WPI; 1998-521232/44.
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Best Local Similarity
Matches 18; Conserv
                     WO9841648-A2
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New human serine/threonine protein kinase 48 and its encoding polynucleotide, useful for treating cancer and human immunodeficiency virus infection -
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/note= "this base represents an unspecified number of
bases"
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                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of ht serime'threonine protein kinase 48. The sequences can be used in the treatment of cancer and HIV infection. The present sequence is a PCR primer for the coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.6%; Score 17.4; DB 1;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                    Example 3; Page 17(Disclosure); 33pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
(BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1082 TTAAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2001; 2001EP-0201936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2002; 2002WO-NL00322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ23536 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                   WPI; 2001-530471/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-129440/12.
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of a gene is involved in preventing a replication error in a cell. The method comprises providing the cell with a specific inhibitor for the groduct and determining the level of functional expression of a marker gene in the cell, where the level of expression of the marker gene in the cell, where the level of expression of the marker gene is dependent on the occurrence of the replication error. The method is preventing a replication error in a cell. The identified genes are useful for developing diagnostic tools, or as targets for drug development to manipulate cells on the basis of the presence or absence of function of the gene. ABZ21535-36 represents fragments of plasmids used to detect somatic instability, in the course of the invention.
                                                                                            The specification describes a method for determining whether a product
Example 1; Fig 3; 47pp; English.
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Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 2 other;

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Length 24;
                                         Indels
   1.6%; Score 17.4; DB 1;
90.0%; Pred. No. 2.2e+02;
live 0; Mismatches 2;
                                                               1081 ATTABABABABABABA 1100
                                                                                               ATGNAAAAAAAAAAAA 20
                Best Local Similarity 90.0
Matches 18; Conservative
Query Match
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Gaps

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AAT94431 standard; mRNA; 19 AAT94431; RESULT 214 AAT94431

(first entry) 02-MAR-1998

Template mRNA poly-A tail SEQ ID NO:1 from W09729211.

Primer; detection; characterisation; mRNA; restriction display PCR; synthesis; cDNA; ss.

Homo sapiens Synthetic

WO9729211-A1

14-AUG-1997

97WO-US02009 07-FEB-1997; 09-FEB-1996; (USSH) US DEPT HEALTH & HUMAN SERVICES.

96US-0011379

Weinstein JN; Boulamwini J,

WPI; 1997-415362/38.

A method has been improved for detecting and characterising mRNA isolacid mRNA includes synthesising a double stranded (ds) cDNA from isolated mRNA, digesting the ds cDNA with a restriction endonuclease to produce cDNA fragments in which at least one end of the cDNA fragments in which at least one end of the cDNA fragments in improvement comprises: (a) hybridising to an adaptor DNA sequence. The one end of the cDNA fragments, (b) ligating the adaptor DNA sequences to the cDNA fragments; (c) amplifying the cDNA fragments having ligated adaptor DNA sequences adaptor bNA sequences of the cDNA fragments; (c) amplifying the cDNA fragments to the ends of the cDNA fragments, where the primers that hybridise to the ends of the cDNA fragments. Detection and characterisation of mRNA by restriction display PCR comprising synthesis of cDNA, digestion with a restriction endonuclease, ligation to an adaptor DNA and PCR amplification Disclosure; Page 24; 40pp; English.

at the 3' end that specifically hybridises to a subset of cDNA molecules; and (d) detecting the presence of the resulting amplified cDNA fragments. The present sequence represent a template poly-A tail used in the present specification. The method designate restriction display PCR can be used for characterising cells based on their mRNA therapeutics that alter cellular gene expression. The method is also useful for characterising cells of a variety of types and under a useful for characterising cells of avariety of types and under a variety of physiological conditions. The method is also useful for identifying cells or tissue from particular individuals or species based on the fingerprint obtained from the mRNA content of isolated cells or tissue and comparing it to cells or tissue from a known source. .; 0 Length 19; 0; Indels 1.6%; Score 17.2; DB 1; 94.4%; Pred. No. 1.9e+02; Sequence 19 BP; 17 A; 0 C; 0 G; 0 U; 2 other; 1; Mismatches 1083 TAAAAAAAAAAAAA 1100 ВАААААААААА Local Similarity 94.4 les 17; Conservative Query Match Matches à

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss. RT-PCR primer of the invention SEQ ID 31. BP. AAX18390 standard; DNA; 19 (first entry) 11-MAY-1999 Synthetic. AAX18390; RESULT 215 AAX18390,

97JP-0208312. 97JP-0208312. JP11032765-A. 18-JUL-1997; 18-JUL-1997;

(TAKI) TAKARA SHUZO CO LTD. WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in RT-PCR

Example 1; Page 12; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-bera-N3'; or (X)m5'-(gamma)k-delta-N3'; where

(X)m5'-(alpha)n-bera-N3'; or (X)m5'-(gamma)k-delta-N3'; where

(M)m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

(M)m = adenine, guanine, cytosine or thymine; gamma = thymine;

(M)m = adenine, guanine, cytosine or thymine; gamma = thymine of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.

Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 2 other;

Gaps ·. Length 19; Indels 1.6%; Score 17.2; DB 1; 94.4%; Pred. No. 1.9e+02; tive 1; Mismatches 0; Query Match 1.6 Best Local Similarity 94.4 Matches 17; Conservative

·.

(first entry)

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Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtaining transgenic plant useful for controlling seed germination ar seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone
                                                                       Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 17; Page 262; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Brown SM, Elich TD,
                                                                                                                                                                                                                                                                                                                                          (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-224351/19.
                                                                                                                                                                           Cucurbita maxima.
                                                                                                                                                                                                       WO200009722-A2
                                         03-JUL-2000
                                                                                                                                                                                                                                                                10-AUG-1999;
                                                                                                                                                                                                                                                                                             10-AUG-1998;
07-JUN-1999;
                                                                                                                                                                                                                                    24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                      Piller KJ,
               AAZ99489;
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nuclectide sequences encoding spearmint

(')-limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3-
bydroxylase (L3H). Host cells containing a vector comprising the
nucleotide sequences can be used for the recombinant production of
limonene hydroxylases or of primary enzyme products. The primary enzyme
limonene hydroxylases or of primary enzyme products. The primary enzyme
limonene hydroxylases or of primary enzyme products are trans-carveol in the case of (-)-L6H or
trans-isopiperitenol in the case of (-)-L3H, which are of subsequent use,
to obtain enhanced expression of limonene hydroxylase in plants to attain
enhanced trans-carveol or trans-isopiperitenol production as a predator
contained production as a predator
limonene hydroxylase cDNAs also provide a useful tool for isolating
other monoterpene hydroxylase genes and for examining the developmental
regulation of monoterpene biosynthesis. Sequences AAX06564-73 represent
primers for the PCR amplification of (-)-limonene-6-hydroxylase cDNAs.
                                                                                                                                                                                                                        (-)-limonene-6-hydroxylase; (-)-limonene-1-hydroxylase; L3H; L6H; spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol; trans-isopiperitenol; pathogen defense mechanism; attractant; environmental signal; monoterpene hydroxylase; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated limonene hydroxylase nucleic acids - which encode limonene-6-hydroxylase and limonene-3-hydroxylase, which can be used to produce trans-carveol and trans-isopiperitenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 17.2; DB 1; Length 19; 94.4%; Pred. No. 1.9e+02; ive 1; Mismatches 0; Indels
                                                             4.72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                              (-)-limonene-6-hydroxylase primer 3.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 27; 80pp; English.
      1083 TAPABABABABABABA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lupien SL;
                                  ВААААААААААААА 1
                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US12581
                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0881784
                                                                                                       AAX06572 standard; DNA; 19
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karp F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-105618/09.
                                                                                                                                                                                                                                                                                                                  Mentha spicata.
                                                                                                                                                                                                                                                                                                                                               WO9859042-A1
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1998;
                                                                                                                                                                  06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Croteau RB,
                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1998
                                                                                                                                                                                                                                                                                                    Synthetic
                                  18
                                                                                                                                    AAX06572;
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                                                                                         AAX06572/
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Loguech SJ;

Logusch EW,

Kishore GM,

Heck GR,

99WO-US18066. 98US-0096111. Ream JE;

Rao S,

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The present primer was used to reverse transcribe cDNA encoding a C-20 oxidase. The amplifie fragment is used in the method of the invention. The specification describes methods for the inhibition and control of gluberallic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberallin biosynthetic pathway sequence, products. The methods uses copaly1 diphosphate synthase, and a peta-hydroxylase, 2-oxidase, phycoene synthase, C-20 oxidase, and a leaf to control seed germination and seedling growth especially to regulate gene products of gibberallin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The products of gibberallin deficient, and have shortened hypocotyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' sequencing primer #1 to identify and characterise polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                          epicotyl phenotypes compared to normal plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 17.2; DB 1;
94.4%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1083 TAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD15201/c
ID AAD15201 standard; DNA; 19 BP
XX AC AAD15201;
XX
XX
XX
XX
DF 01-NOV-2001 (first entry)
DE 3' sequencing primer #1 to id
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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Gaps

; 0

1083 TAAAAAAAAAAAAA 1100

17; Conservative

Matches

Local Similarity

N

DAAAAAAAAAAAAAA

19

q à

AAZ99489 standard; DNA; 19

RESULT 217 AAZ99489/c ID AAZ9949

gene therapy;

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nervous system disorder; Parkinson's disease; immune system disorder; ischaemia; lymphopsenia; leukocyte adhesion deficiency syndrome; haemoglobinuria; anaemia; hyperproliferative disorder; daucher's disease; coagulation disorder; blood platelet disorder; autoimmune disorder; dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis; drave's disease; gene therapy; antiarteriosclerotic; immunostimulant; cardiovascular; antiviral; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency syndrome or haemoglobinuria, anaemia), hyperproliferative disorders (e.g. Gaucher's disease), infectious disease (e.g., herpes simplex), coagulation disorders, blood platelet disorders and autoimmune disorders. The polynucleotide sequence is also used in gene therapy. The present sequence is a 3 sequencing primer used in the identification and characterisation of polynucleotides up-regulated by fatty lesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an isolated nucleic acid regulated by fatty lesion development, which comprises any of 55 polynucleotide sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or antibody is useful for preventing, treating, modulating or ameliorating a medical condition, particularly atherosclerosis. The invention is used as a marker or detector of nervous system disorder or disease (e.g. Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The invention may also be useful for treating deficiencies or disorders of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides regulated by fatty lesion development and their encoded polypeptides, useful for preventing, treating or ameliorating atherosclerosis, as well as for immune or hyperproliferative disorders
      atherosclerosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glass JR, Sutcliffe JG, Hasel KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DB 1;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 79; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1083 TAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US02439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 94.4%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000; 2000US-0177963
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sartani A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514526/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                               WO200154651-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonardi A,
                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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Matches
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0
                                                                                                                                                                                                                                                                Mouse; microglia; macrophage; regulatory gene; digital sequence tag;
DST; PCR-based total gene expression analysis; TOGA; infectious disorder;
                            Gaps
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0
Length 19;
                                                                                                                                                                                                                                   Mouse microglia and macrophage regulatory gene primer #60.
                         Indels
                                                                                                                                                 AAS06525 standard; DNA; 19
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                        07-SEP-2001
                                                                                                                                                                              AAS06525;
                                                                                                                     RESULT 219
                                                                                                                                    AASO6525/,
ID AASO
XX
XX AASO
DT 07-SJ
XX
DE MOUS'
XX
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The present sequence is presents a pixture used to isolate involved mouse microglia and macrophage regulatory gene DST (digital sequence tag) sequences. AAS06401-AAS06590 represent these novel sequences and the primer sequences used to isolate them. The PCR-based total gene expression analysis (TOSA) system is used to examine the expression pattern of molecules corresponding to genes that are regulated in continulated microglia, unstimulated macrophage. The polynucleotides of the invention, the polypeptides are useful for the diagnosis, prevention, treatment or amelioration of a medical condition, preferably a neuroinflammatory pathology or a neurodegenerative disease such as polypeptides are useful for the diagnosis, prevention, treatment or amelioration of a medical condition, preferably a neuroinflammatory pathology or a neurodegenerative disease such as Alzheimer's disease, senile dementia, Parkinson's disease, obsessive depression and bipolar manic-depressive disorder. The sequences and metotious disorders (e.g. ADDS), hyperproblicating or treating contrections disorders (e.g. ADDS), hyperproblication of disorders (e.g. severe combined immunodeficiency, SCID) autoimmune diseases (e.g. insulin dependent diabetes mellitus), infinammatory disorders (e.g. insulin dependent diabetes mellitus), infinammatory disorders (e.g. insulin dependent diabetes mellitus), infinammatory disorders (e.g. arthritis). The polynucleotides can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; human; total gene expression analysis; TOGA; DST; EST; digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          New regulated genes of microglia and macrophages, useful for diagnosing, preventing or treating neuroinflammatory pathology and neurodegenerative disease
neuroinflammatory pathology; neurodegenerative disease; gene the hyperproliferative disorder; autoimmune; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a primer used to isolate novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 17.2; DB 1; Length 19; 94.4%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Almazan MT,
                                                                                                                                                                                                                                                                                                                     DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 88; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 TAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                      12-NOV-1999; 99WO-US26824.
03-MAR-2000; 2000US-0186770.
19-JUN-2000; 2000US-0212465.
                                                                                                                                                                                                   06-NOV-2000; 2000WO-US30585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH21968 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                               Sutcliffe JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for gene therapy
                                                                                                                    WO200134770-A2.
                                                                                 Mus musculus.
                                                                                                                                                            17-MAY-2001.
                                       primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                             Carson MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH21968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH21968/
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Makakakaka
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Thu Jan

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us09904568-1.rng

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The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (I), polypeptides (II) comprising (I), are useful for encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition to such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosting a pathological condition or susceptibility to a schizophrenia, a bipolar disorder or addiction-related behaviour. (I) are useful for detecting the presence of a nucleic acid encoding a protein caseful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple choiced isometers in the control gene expression through triple above mentioned disorders, indentifying individuals from minute to biological samples, as an alternative to restriction fragment length collymorphism (RPLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, call type, as a probe to subtract-out known sequences in the process of discovering novel polymucleotides, for selecting and making oligomers of for attachment to a gene chip or other support; to ratae anti-out propher and as an anti-out probe and and as an anti-out probe and and as an anti-out probe and as an anti-out probe and and and any probe and and any probe and an anti-out probe and and any probe and an
central nervous system; antidepressant; gene therapy; diagnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addiction-related behaviour; chromosome identification; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New neuroleptic-regulated polymucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B,
                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 87; 210pp; English.
                                                                                                                                                                                                                                                                                                                       26-OCT-2000; 2000WO-US29690
                                                                                                                                                                                                                                                                                                                                                                                    99US-0161379
                                                                                      PCR primer; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-300499/31
                                                                                                                                                                                                     WO200130972-A2
                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-1999;
                                                                                                                                                                                                                                                               03-MAY-2001
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Gaps
                                                ó
                      Score 17.2; DB 1; Length 19;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                             0; Indels
Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                          1,
                      1.68;
                                           Conservative
                               Local Similarity
                                         17;
                    Query Match
                                        Matches
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1100
                  7
1083 TAAAAAAAAAAAAAA
                19 ВАААААААААААААА
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AAF76617 standard; DNA; 19
                                   AAF76617
RESULT 221
AAF76617/C
ID AAF7/
XX
AC AAF
XX
DT 7
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ВÞ

(first entry) 15-MAY-2001

Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.

WPI; 2002-489107/52

Piller KJ,

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The present invention provides the protein and coding sequences of the peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)-limonene-6-hydroxylase. Also provided are a number of probes and PCR primers which were used to isolate the sequences. These are useful in the production of transgenic plants with altered flavour and aroma.
                                                                                                                                                                                                                                                                                                          Novel isolated limonene hydroxylase encoding nucleic acid molecule, useful for altering production of limonene-6-hydroxylase or limonene-3-hydroxylase in suitable host cell -
                                     SS.
             Spearmint; peppermint; (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                          Example 4; Column 55; 57pp; English
                                                                                                                                                       99US-0292768
                                                                                                                                                                                                                                                Croteau RB, Lupien SL,
                                                                                                                                                                                                                                                                               WPI; 2001-243405/25.
                                                          Mentha spicata.
                                                                                        US6194185-B1
                                                                                                                                                    14-APR-1999;
                                                                                                                     27-FEB-2001,
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Hasel KW;

1083 TAAAAAAAAAAAAA 1100 ~ DAAAAAAAAAAAAA 19 à d

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Gaps

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Mismatches

1,

17; Conservative

Local Similarity

Matches

Query Match

Length 19; Indels

1.6%; Score 17.2; DB 1; 94.4%; Pred. No. 1.9e+02;

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Gibberellin; transgenic plant; seed germination; seedling growth; GA,
transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
                                                                                                                                                                                                                 HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
                                                   AAD40279 standard; DNA; 19
                                                                                                                                                                   (first entry)
                                                                                                                                                                   22-OCT-2002
                                                                                                            AAD40279;
RESULT 222
                               AAD40279,
```

Loguach SJ; Logusch EW, Kishore GM, Elich TD, Heck GR, Rao S, Ream JE; 99US-0371307. 99US-0371307 (BROW/) BROWN S M. US2002053095-A1 Cucurbita pepo 10-AUG-1999; 10-AUG-1999; 02-MAY-2002 Brown SM, THE STANTANT OF THE STANTANT O

The invention relates to control of gibberellin (GA) levels in plants.

The method involves producing transgenic plants having a phenotype of reduced seed germination and early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of permination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is a per primer is used in the exemplification of the invention Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other; Example 19; Page 104; 155pp; English. restore these properties

1.6%; Score 17.2; DB 1; Length 19; 94.4%; Pred. No. 1.9e+02; iive 1; Mismatches 0; Indels 1083 TAAAAAAAAAAAA 1100 0 Best Local Similarity 94.4 Matches 17; Conservative Query Match à

ВААААААААААААА 13

ABQ73231 standard; DNA; 19 BP. ABQ73231; RESULT 223

(first entry) 27-SEP-2002

Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.

Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia; TOGA primer; ss.

Oryctolagus cuniculus, Synthetic.

WO200242420-A2.

30-MAY-2002

21-NOV-2001; 2001WO-US44072

21-NOV-2000; 2000US-252216P

Hasel KW; (DIGI-) DIGITAL GENE TECHNOLOGIES INC. Glass JR, Sartani A, Leonardi A,

WPI; 2002-575233/61.

New polynucleotides related to regulated genes characteristic of atherosclerosis, useful for diagnosing, preventing, treating, modulating or ameliorating atherosclerosis in a mammalian subject

Disclosure; Page 28; 130pp; English.

and its The present invention describes an isolated polynucleotide (I) and it complements, and degenerate variants, comprising a sequence selected

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sequence tag (DST) corresponding to many.sazz (NS), which is a digital sequence tag (DST) corresponding to many.sazz (NS), which is regulated by proliferative lesion development caused by mechanically induced intimal hyperplasia, or by lercanidipine treatment. Or by proliferative lesions and reversed by lercanidipine treatment. (I) has antiatherosclerotic activity and can be used in gene therapy. (I) can be used for diagnosing a medical condition (e.g. atherosclerosis) in a subject which involves determining the presence or absence of a mutation in (I) and diagnosing the medical condition based on the presence or absence or absence or absence of a mutation in (I) and diagnosing the medical condition based on the presence or absence or an order or an increase or decreases) in an anterosclerosis, or the susceptibility to atherosclerosis in a subject with dihydropyridine monitoring the effects of treating a subject with dihydropyridine preventing, treating, modulating, or ameliorating a medical condition research invariant which is used in the exemplification of the research invariant.
   to ABQ73222 (NS), which is a digital
      in ABQ73206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
   those given
$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Gaps 0; Length 19; 0; Indels 1.6%; Score 17.2; DB 1; 94.4%; Pred. No. 1.9e+02; 1; Mismatches Local Similarity 94.4 Query Match Matches

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1083 TAAAAAAAAAAAAA 1100 19 ВААААААААААААА

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Gaps

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RESULT 224

ABK71509 standard; DNA; 19 ABK71509,

BP.

ABK71509;

(first entry) 30-JUL-2002

CNS related 3' sequencing primer.

Central nervous system, CNS; neuroleptic; mouse; human; psychoses; neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease; Pick's disease; senlle dementia; encephalopathy; Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia; addiction; multiple sclerosis; depression; manic-depressive disorder; primer; ss.

Synthetic.

WO200226936-A2.

04-APR-2002.

01-OCT-2001; 2001WO-US30695.

29-SEP-2000; 2000US-236790P. 18-JAN-2001; 2001US-263084P.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Hasel KW; Hilbush BS, Pribyl TM, Sutcliffe JG, Thomas EA,

WPI; 2002-383271/41.

New polynucleotide useful in gene therapy for preventing, treating modulating or ameliorating a medical condition such as psychoses or a neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a mammal

Example 1; Page 40; 254pp; English.

This invention relates to the cDNA sequences of novel isolated

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polymucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D 2 creeptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the cor ameliorating a medical condition e.g. a neuropsychiatric disorder. An preventing, treating, modulating or ameliorating neurological disorders or such as psychoses or other neuropsychiatric disorders in a subject. The succeptibility to a neurological disorders or a succeptibility to a neurological disorders or such as psychoses or other neuropsychiatric disorders in a subject. The succeptibility to a neurological disorders such as psychoses and other conceptibility to a neurological disorders in a subject by determining the presence or succeptibility to a neurological disorders in the expression of determining the alteration (increase or determining the proliferation (conceptible propertion). The sequences of the invention are useful in treating nervous system by activating or inhibiting the proliferation.

Confidential calls. The sequences are useful as a marker, or determining or inhibiting the proliferation.

Confidential calls. The sequences are useful as a marker or determining or inhibiting the proliferation.

Confidential calls. The sequences are useful as a marker of disease, bick's disease, binswanger's disease, other senile demenia, addiction, multiple sclerosts, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosts, depression and manic-depressive disorders. The present sequence represents an extension of the invention of the contrains of the Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other; the invention. 8\$

Gaps · 0 Query Match
1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels

1083 TAAAAAAAAAAAA 1100 N 19 вададададададада

ð g AAD34663 standard; DNA; 19

AAD34663;

BP.

(first entry) 16-JUL-2002

PCR primer #4 used for direct sequencing of TOGA generated PCR products. Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide; acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease; TOGA; TOtal Gene expression Analysis; PCR; primer; ss.

Unidentified

WO200222783-A2

21-MAR-2002.

15-SEP-2000; 2000US-233176P. 17-SEP-2001; 2001WO-US29123

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Hilbush Mueller R, Guidotti LGDVM, Wieland SF, WPI; 2002-339865/37. Chisari FV,

Preventing and treating hepatitis viral infection in a mammal, comprises administering nucleic acid molecules that up- or down-regulate in hepatitis B virus infection or polypeptides encoded by the nucleic acid molecules

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The present invention relates to a method for preventing, treating, modulating or ameliorating a medical condition. The method involves administering one or more nucleic acid molecules up- or down-regulated in hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic acid molecules or antibodies that bind to the polypeptide. The method is useful for preventing, treating, modulating or ameliorating or a medical condition. It is also useful for determining the presence or alteration in expression of the polypeptide which is useful for the diagnosis of hepatitis viral infection. The method is useful for the assessing the stage of hepatitis viral infection (e.g., acute hepatitis viral infection (e.g., acute hepatitis or therapeutic treatment for hepatitis viral infection and a gene expression profile is useful for identifying polypeptides and polymucleotides which are used in gene therapy and as vaccines. Nucleic acid sequences are consecuted with hepatitis viral infection. Sequences of the invention are useful as a diagnostic markers for HBV infection and for treating infectious diseases. The present DNA sequence is a PCR primer which is useful and product and approach and a general and a product are associated with hepatitis viral infection and for treating infectious diseases. The present DNA sequence is a PCR primer which are also and a product and approach and a product and and a product and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 17.2; DB 1;
4.4%; Pred. No. 1.9e+02;
ve 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
Disclosure, Page 28; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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~ BP. 19 вададададададада ABZ68389 standard; DNA; 19 RESULT 226 g

1083 TAAAAAAAAAAAAA 1100

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ABZ68389,

(first entry) 22-APR-2003 ABZ68389;

Reverse transcription primer used to produce yeast cDNA.

Histone acetyltransferase; histone deacetylase; gene expression profile; chromatin-associated protein; gene expression; primer; ss.

Synthetic.

WO2003000715-A1.

03-JAN-2003

21-JUN-2002; 2002WO-US19750.

22-JUN-2001; 2001US-300135P.

(CERE-) CERES INC.

Dang V, Okamuro J;

WPI; 2003-175280/17.

New chimeric polypeptide comprising a histone acetyltransferase polypeptide segment and a segment comprising a histone deacetylase chromatin-associated protein complex subunit, useful for modulating gene expression in cells -

Example 10; Page 54; 85pp; English.

The specification describes chimeric histone acetyltransferase polypeptides. The chimeric polypeptides comprise a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide

us09904568-1.rng

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Gaps

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0; Indels

Mismatches

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Length 19;

Page 102

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The present invention relates to a novel simplified TOGA (RTM) method for simultaneous sequence-specific identification of multiple mRNA molecules in a RNA population. The method involves charactrising each of the sequence-specific polymerase chain reaction (PCR) products by partial patterns of gene expression or mechanisms of drug interaction. It is also useful for drug screening, studying physiological processes, genomic The present sequence of diagnostic, prognostic or therapeutic reagents invention.
               histone deacetylase chromatin-associated protein complex. The chimeric polypoptides are useful for determining gene expression profiles in specific cells, for modulating gene expression in specific cells, and for making genetically modified eukaryotes. The present sequence represents a reverse transcription primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 3' sequencing primer #1 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene expression; drug interaction mechanism; drug screening; primer; genomic mapping; ss.
segment having 40% or greater sequence identity to a subunit of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simplified TOGA method for simultaneous sequence-specific identification of multiple mRNA molecules in mRNA population, for determining tissue-specific patterns of gene expression or mechanisms of drug interaction -
                                                                                                                                                              1.6%; Score 17.2; DB 1;
94.4%; Pred. No. 1.9e+02;
                                                                                                                            Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIGITAL GENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39; 93pp; English.
                                                                                                                                                                                                                         1083 TAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasel KW,
                                                                                                                                                                                                                                                       19 ВААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2002; 2002WO-US02666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2001; 2001US-0775217
                                                                                                                                                                                                                                                                                                                                     AAD50267 standard, DNA, 19
                                                                                                                                                     Query Match
Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quan J, Hilbush BS,
Callahan MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-092784/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200261045-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2002
                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                     AAD50267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIGI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (QUAN/)
                                                                                                                                                                                                                                                                                                        RESULT 227
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The invention relates to polynucleotides and polypeptides associated with atherosclerosis. Polynucleotides of the invention are useful for delivery of genes, DNA vaccines, diagnostic reagents, peptides, for treating nervous system disorders of the invention are useful for treating nervous system disorders (e.g., Alzheimer's disease, continued associated for treating nervous system disorders (e.g., Alzheimer's disease, parkinson's disease, multiple sclerosis, epilepsy), immune disorders (e.g., autoinmune disorders such as rheumatoid arthritis, Addison's disease, haemolytic anaemia, graft-versus-host disease, inflammation), hyperproliferative disorders (e.g., neoplasms) and infectious diseases (e.g., viral, bacterial, fungal or parasite infection). They are used to resensation of tissues, to repair, replace or protect damage tissues, for increasing chemotaxis activity of cells, for increasing chemotaxis activity of cells, for increasing chemotaxis activity of cells, for increasing chemotaxis activity of cells for increasing calls from a lineage, for modulating mammalian characteristics, (such as body weight or height), for modulating mammalian metabolism and storage of energy, to change a mammal's mental or physical state, or as a food additive or preservative. The invention is useful in gene therapy. The modulating is the invent seminarion.
                                                                                                                                                                                                                                                                                                                                Parkinson's disease, multiple sclerosis; immune disorder; gene therapy; autolimune disorder; rheumatoid archritis; hyperproliferative disorder; haemolytic anaemia; graft-versus-host disease; inflammation; infection; epilepsy; Addison's disease; heoplasm; tissue regeneration; chemotaxis; food additive; food preservative; primer; ss.
                                                                                                                                                                                                                                                                                                               Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide associated with atherosclerosis, useful for treating atherosclerosis, nervous system disorders, immune disorders, hyperproliferative disorders and infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is a sequencing primer used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hasel KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutcliffe JG,
                                                                                                                                                                                                                                                                     3' sequencing primer #1 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 139, 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glass J,
1083 TAAAAAAAAAAAAA 1100
                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2000; 2000US-248892P.
28-NOV-2000; 2000US-253623P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-2001; 2001WO-US43741
                                                                                                                                                   13
                                                                                                                                                                                                                                (first entry)
                                                                                                                                            AAD49149 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leonardi A, Sartani A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-058561/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200281726-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                             07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-0CT-2002,
                                                                                                                                                                                      AAD49149;
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Gaps

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1.6%; Score 17.2; DB 1; Length 19; 14.4%; Pred. No. 1.9e+02; ve 1; Mismatches 0; Indels

94.48;

Conservative

Local Similarity Les 17, Conserva

Matches

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Gaps

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Query Match 1.6%; Score 17.2; DB 1; Length 19; Best Local Similarity 94.4%; Pred. No. 1.9e+02; Matches 17; Conservative 1; Mismatches 0; Indels

Query Match

useful

Chang HW;

Sutcliffe GJ,

1083 TAAAAAAAAAAAAA 1100

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Analysis of DNA fragment - comprises addition of known common oligonuclectide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA
                                                                                     Primer; DNA analysis; amplification; hybridisation; ss.
                                                                        Oligonucleotide 9 for DNA analysis.
                                                                                                                                                                                                                 Example 5; Page 12; 17pp; Japanese.
98JP-0005399.
                                                                                                                                                   98JP-0005399.
                                     AAZ09197 standard; DNA; 20
                                                              (first entry)
                                                                                                                                                                            WPI; 1999-496652/42.
                                                                                                                                                               (HITA ) HITACHI LTD.
                                                                                                             JP11196874-A.
                                                             19-0CT-1999
                                                                                                                                       14-JAN-1998;
                                                                                                                                                   14-JAN-1998;
                                                                                                                         27-JUL-1999.
                                                                                                  Synthetic.
                                                 AAZ09197;
      19
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This invention describes a novel method for the analysis of a DNA fragment which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment, (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence, a second common primer containing a complementary nucleotide sequence to the prepared known common oligonucleotide sequence at a terminal, and a specific primer complementary nucleotide sequence at a terminal, and a specific primer complementary nucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the gene having known sequence, to give amplified DNA, (iii) cragable of the amplified DNA to find the information of the DNA cragment, in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of the common first and second primers and to give short fragment of Differentiation of informations of known and unknown genes readily signals derived from minor genes can be performed. AAZ09189-Z09201 crepresent oligonucleotide primers used to illustrate the method

Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 2 other;

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Score 17.2; DB 1; Length 20;
Pred. No. 2e+02;
1; Mismatches 0; Indels
                                                 1100
            94.48;
                                              1083 TAAAAAAAAAAAAAA
                        17; Conservative
          Local Similarity
Query Match
                      Matches
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Gaps

RESULT 230
AAC69376
ID AAC6937
XX

19 ВАААААААААААААА

AAC69376 standard; DNA; 22 BP.

29-JAN-2001 (first entry)

AAC69376;

Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.

high density lipoprotein; Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotes
Tangler disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diaprognosis; prophylaxis; drug screening; transgenic animal; ds.

Homo sapiens.

WO200055318-A2.

21-SEP-2000

15-MAR-2000; 2000WO-IB00532

99US-0124702, 99US-0138048, 15-MAR-1999;

99US-0139600. 08-JUN-1999; 01-SEP-1999;

Pimstone SN; (UYBR-) UNIV BRITISH COLUMBIA (XENO-) XENON BIORESEARCH INC Wilson AR, Hayden MR,

WPI; 2000-587528/55.

New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

Examples; Fig 11; 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein

(B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

a member of the ATP-binding cassette (ABC transporter) superfamily of

proteins, and plays a crucial role in cholesterol transport, particularly

intracellular cholesterol trafficking in moncoytes and fibroblasts, being

convolved in cholesterol efflux from the cell. The gene encoding ABC1 is

located on chromosome 9431, and mutations in this gene are associated

with two genetic HDL (high density lipoprotein) deficiency disorders,

Tangier disease (TD) and familial HDL deficiency (FHA). These diseases

care distinguishable in that TD is an autosomal recessive disorder, while

FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good

cholesterol") in the blood correlate with a high risk of cardiovascular

cdisease, particularly coronary artery disease, but also cerebrovascular

characteristic and peripheral vascular disease. cerebrovascular disease, coronary restenosis or peripheral viscular disease. They may also be used in the treatment of disease associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAAl0005.1 and X75926, and the nucleic disease, coronary restenosis, and peripheral vascular disease.

Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABCI nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABCI or an active fragment thereof. The invention also encompasses compounds which mimic ABCI activity, compounds which encompasses compounds which mimic ABCI activity, compounds which stimulate ABCI expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease,

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RESULT 232
                             AAD51324,
                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a method for producing a molecular array, the method involves immobilising molecules to a solid phase at a density which allows individual immobilised molecules to be individually resolved. The molecular array produced by the method of the invention is useful for identifying one or more target molecules in a sample. The studies, is also useful in genetic analysis, gene expression studies, identifying molecules which interact with a target molecule, detection/typing of single nucleotide polymorphisms, haplotyping and sequencing. The present DNA sequence represents a PCR primer that was
                                                                                                                                                                                                                                                                                        ss; target molecule identification; genetic analysis; SNP detection; haplotyping; sequencing; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing a molecular array with a plurality of molecules immobilized to a solid substrate, useful in genetic analysis, gene expression studies or the detection or typing of single nucleotide polymorphisms in a sample of nucleic acids
                                                                                              Gaps
acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1
                                                                                              ..
                                                                     Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.6%; Score 17.2; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 1; Mismatches 0; Indels
                                                                                            Indels
                                                                                                                                                                                                                                                                    Molecular array production method-related PCR primer.
                                                                   1.6%; Score 17.2; DB 1;
86.4%; Pred. No. 2.2e+02;
Live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.
                                              Sequence 22 BP; 6 A; 2 C; 11 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 15; Page 122; 166pp; English.
                                                                                                                 991 TIGGAAGICIGAGGCIGGAGAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in an example of the invention.
                                                                                                                                        22
                                                                                                                                       1 Tregenegerenegeczeczen
                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2002; 2002WO-GB01245.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2001GB-0018879.
                                                                                                                                                                                                                                                                                                                                                                                                                       2001GB-0006635
                                                                                                                                                                                                AALS0570 standard; DNA; 22
                                                                                                                                                                                                                                              (first entry)
                                                               Query Match
Best Local Similarity 86.4:
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-732872/79.
                                                                                                                                                                                                                                                                                          Molecular array;
gene expression;
                                                                                                                                                                                                                                                                                                                                                  WO200274988-A2.
                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001;
                                                                                                                                                                                                                                            12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2002.
                                                                                                                                                                                                                        AAL50570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mir K;
                       gene.
                                                                                                                                                                         RESULT 231
                                                                                                                                                                                    AAL50570/c
82888
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The internation of a performance animal. The method involves determining in sample abundance of expressed target nucleic acid; transmitting digital sample signal to remote diagnostic server; processing digital sample signal at remotely located database to correlate digital signal with digital information and returning report of particular condition of animal. The method is useful for assessing a condition of a performance animal preferably human, dog or camel. The condition can be an athletic ability and a condition that enhances, hinders, impedes or does not change an expected ability of the performance animal; and also normal, pre-clinical, overt progress and/or stage of disease, undiagnosed of unclassified conditions, presence of drugs, response to environmental conditions. Diseases nutritional states and response to environmental conditions. Diseases assessed by the invention include laminitis, lameless, viral or bacterial disease, gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis, musculoskeletal damage or disorders and joint diseases. The presence is a primer used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                            Laminitis, viral disease, vaccine, bacterial disease, primer, epistaxis, gastritis, gastric ulcer, respiratory ailment, fracture, joint disease, musculoskeletal damage, ss.
                                                                                                                                                                                                          Anchored oligo dT primer used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assessing condition e.g. athletic ability, stage of disease, presence of drugs, response to exercise, response to vaccines, therapies, nutritional states, of performance animal involves analyzing nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for assessing a condition of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOMICS RES PARTNERS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 46; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1083 TAAAAAAAAAAAAA 1100
AAD51324 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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29-JUN-2001; 2001US-0896941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2002; 2002WO-AU00553.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-120558/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
Les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200290579-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                        16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandon RB;
                                                                  AAD51324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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ID ABX748
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New microarray, comprising a matrix of cDNA probe from a set of probes immobilised to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma
                                                         Microarray; solid surface; immobilised probe; CC-RCC; differential expression profile; aggressive CC-RCC tumour type; non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; oligo-dT; primer; ss.
                                       Oligo-dT primer used in human CC-RCC invention.
                                                                                                                                                                                                                                                                                                        Example 2; Page 30; 179pp; English.
                                                                                                                                                                  29-MAR-2002; 2002WO-US09576.
                                                                                                                                                                                      29-MAR-2001; 2001US-279411P
                                                                                                                                                                                                                              Teh BT,
                    (first entry)
                                                                                                                                                                                                        (VAND-) VAN ANDEL INST
                                                                                                                                                                                                                                               WPI; 2003-040679/03
                                                                                                                                                                                                                            Rhodes D,
                                                                                                                            WO200279411-A2.
                    21-MAR-2003
                                                                                                                                                10-OCT-2002
                                                                                                          Synthetic
 ABX74887;
                                                                                                                                                                                                                            Haab B,
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Takashi M;

The present invention relates to a microarray comprising a matrix of at least one CDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to nucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal acarcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the prognosis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence represents an oligo-dT primer used in the examples of the Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other; Query Match Best Local Similarity

Gaps · 0 1.6%; Score 17.2; DB 1; Length 22; 94.4%; Pred. No. 2.2e+02; Ive 1; Mismatches 0; Indels 94.48; 17; Conservative Matches

1083 TAAAAAAAAAAAAA 1100 21 вададададададада

g à

ABK13916 standard; DNA; 23 BP 21-MAY-2002 ABK13916;

3'-PCR primer used in method of identifying transcribed genes. (first entry)

Identification of transcribed gene; mRNA profile; gene expression; cellular process; fingerprinting; susceptibility to external factor; development; disease; PCR; primer; ss.

mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules present in a sample and analysing the patterns of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes having a role in various cellular processes. The method is useful for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes. Including susceptibility to external factors, development, and disease. The present sequence for a PCR primer is used in the methods of the present invention. comparing Providing mRNA profile, by generating two independent patterns characteristic of sample mRNA population, analysing patterns, comparing gene expression by cell types under varied conditions, and identifying present invention relates to a method for providing a profile Seguence 23 BP; 0 A; 0 C; 0 G; 20 T; 3 other; Bauren G; Example 2; Page 45; 67pp; English. 21-JUL-2000; 2000GB-0018016. 21-JUL-2000; 2000US-219925P. 23-JUL-2001; 2001WO-IB01539. (GLOB-) GLOBAL GENOMICS AB. Ernfors P, WPI; 2002-217065/27. WO200208461-A2. Linnarsson S. 31-JAN-2002 Synthetic.

븅

Score 17.2; DB 1; Length 23; Pred. No. 2.3e+02; 1; Mismatches 0; Indels Indels 1083 TAAAAAAAAAAAAA 1100 4 1.6%; 94.48; ВАААААААААААА 17; Conservative Local Similarity 21 Query Match Matches à g

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Gaps

0;

ABS55943 standard; DNA; 24 ABS55943; RESULT 235 ABS55943 ID ABS5

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BP.

DNA topoisomerase II (TOP2) 21.34 cDNA RT-PCR primer #2. 22-JAN-2003 (first entry)

cancer; RT-PCR; DNA topoisomerase II 21.34; TOP2; primer; ss; DNA recombination; malignant tumour; haemopathy; human immunodeficiency virus; HIV; immunological disease; inflammation; development disturbance; reverse transcriptase

Inidentified,

CN1345941-A.

24-APR-2002

29-SEP-2000; 2000CN-0125577.

29-SEP-2000; 2000CN-0125577.

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11年 11月 11日

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The invention relates to the polypeptide DNA topoisomerase II (TOP2) 21.34, a polymucleotide encoding the polypeptide and a method for producing the polypeptide by DNA recombination technology. The polypeptide is used for curing several diseases, such as malignant polypeptide is used for curing several diseases, such as malignant twincurs, haemopathy, development disturbance, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. This sequence represents a reverse transcriptase PCR (RT-PCR) primer used in isolation of CDNA encoding DNA topoisomerase II (TOP2) 21.34.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                         New polypeptide-DNA topoisomerase II (Top2) 21.34 for treating malignant tumour, haemopathy, development disturbance, human immunodeficiency virus infection, immunological disease and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to the DNA and protein sequences of leukemia related protein 24.09. The invention also comprises methods for producing the protein using recombinant DNA technology and antagonists of the protein which may be used for inhibiting the action of the protein. The sequences of the invention may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 17.2; DB 1; Length 24; 86.4%; Pred. No. 2.46+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukaemia related protein; leukaemia; lymphoma; primer; ss;
haemopathy; growth development disturbance disease;
reverse transcription; RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukaemia related protein 24.09 specific RT-PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 17 (disclosure); 32pp; Chinese.
                                                                                                                                                                                         Example 2; Page 18 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEV CO LTD.
               (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel leukemia related protein 24.09 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 CAGAGAAGCTGTGGAACTT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CAGAGCAGCTGCGGAGCGACTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2000; 2000CN-0125055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK91269 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                      New polypeptide-DNA malignant tumour, had
                                                                              WPI; 2002-539340/58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-520722/56.
                                               Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK91269;
                                             Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mao Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel human actin similar protein 56.43, polymocleotides encoding the polypeptide and a DNA recombination process to produce the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such a periodic palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes, tumours, etc. The present invention also discloses the antagonist resisting the polypeptide and its treatment effect. This sequence represents a RT-PCR primer used in the amplification of the human actin similar protein 56.43 described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                   actin similar protein 56.43; palsy; arrhythmia; bronchial asthma; ulcer; diabetes; tumour; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide-human actin similar protein 56.43 for treating periodic palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes, and tumors
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
   for treating several diseases such as leukaemia, lymphoma, other haemopathy and growth development disturbance disease. The present sequence represents a reverse transcription (RT) PCR primer used to isolate the leukaemia related protein CDNA 24.09 of the invention.
                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                 Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 17.2; DB 1; Length 24; 86.4%; Pred. No. 2.4e+02;
                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                   Human actin similar protein 56.43 RT-PCR primer #2
                                                                                                              ch 1.6%; Score 17.2; DB 1;
1 Similarity 86.4%; Pred. No. 2.4e+02;
19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 20 (Disclosure); 35pp; Chinese.
                                                                              Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                            1079 CTATTAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATTAAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA.
                                                                                                                                                                                                          CAATTGAAAAAAAAAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crcrrcaaaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000; 2000CN-0119737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2000; 2000CN-0119737
                                                                                                                                                                                                                                                                        :045/c
ABQ76045 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-472210/51.
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                     30-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CN1339501-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2002
                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                       ABQ76045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1079
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                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
peptic
                                                                                                                                            Matches
                                                                                                                                                                                                                                                      RESULT 237
                                                                                                                                                                                                                                                                   8886666
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238

RESULT

Thu Jan

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Aminopeptidase; primer; ss; food composition; dough; flavour enhancer; baked product; cheese; poly-T; reverse transcriptase PCR.
                                                                                                                                                                                                           An isolated polypeptide with aminopeptidase activity, for preparing food compositions, such as bread and cheese, with enhanced flavouring
                                                 Aspergillus niger aminopeptidase RT-PCR primer poly-T.
                                                                                                                                                                                Schuurhuizen PW,
                                                                                                                                                                                                                                 Example 5; Page 40; 94pp; English.
      ABK48140 standard; DNA; 24 BP.
                                                                                                                                  22-AUG-2001; 2001WO-EP09925
                                                                                                                                                 23-AUG-2000; 2000EP-0202995
                                     (first entry)
                                                                                                                                                                               Dekker PJT,
                                                                                                                                                                                             WPI; 2002-257917/30
                                                                                                     WO200216618-A1.
                                                                                                                                                                (STAM ) DSM NV
                                    18-JUN-2002
                                                                                       Synthetic.
                                                                                                                                                                               Basten D,
                     ABK48140;
ABK48140/c
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The invention relates to an isolated polypeptide with aminopeptidase activity and the gene encoding it (including sequences complimentary to the gene and which hybridise to it at high stringency), from Aspergillus niger. Also included are a nucleic acid construct comprising the above miger. Also included are a nucleic acid construct comprising the above for direct the production of the polypeptide in a suitable expression host, a recombinant expression vector comprising the above uncleic acid construct, a recombinant host cell comprising the above construct or recombinant host cell to produce a supernatant and/or cells comprising the polypeptide and recovering the polypeptide. The aminopeptidase is consect to prepare a food composition such as dough to enhance the flavour. The invention provides a bacterial enzyme for protein aperdous is in with aminopeptidase activity, to produce flavouring a previously observed weak aminopeptidase activity which was detected a protein and appropriate or latentification is latent and a produce flavouring a previously observed weak aminopeptidase activity which was never isolated or identified. The use of erzymes to produce flavouring agents from proteinaceous material is better than use of strong acids which is a reverse transcriptore of the amino acids obtained. The present sequence is intron-error error. intron-exon structure of the aminopeptidase gene.

Gaps ó: Length 24; 0; Indels 1.6%; Score 17.2; DB 1; 94.4%; Pred. No. 2.4e+02; tve 1; Mismatches 0; Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 1 other; 94.48; 17; Conservative Similarity Query Match Best Local Matches

0,

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ВРАВВВВВВВВВВ
24
                      RESULT 239
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1083 TAAAAAAAAAAAAA 1100

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ABA04737 standard; DNA; 24 BP
                                    ABA04737;
ABA04737/c
ID ABA047
XX
AC ABA047
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Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2. Human, alkylation DNA protein cysteine methyltransferase 11; cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy; tumour; haemopathy; HIV infection; immunological disease; inflammation; (first entry) PCR primer; 88 WO200188146-A1 Homo sapiens

22-NOV-2001

26-MAR-2001; 2001WO-CN00464 28-MAR-2000; 2000CN-0115226 (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Xie Y; Mao Y,

WPI; 2002-055701/07.

Visser J;

Schaap PJ,

Human alkylation-DNA-protein cysteine methyltransferase and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation -

Example 2; Page 19; 40pp; Chinese.

The present invention relates to human alkylation-DNA-protein cysteine methyltransferase (see AAM47739). The protein and its coding sequence are useful in the diagnosis and treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in an example from the present invention.

Sequence 24 BP; 4 A; 0 C; 4 G; 16 T; 0 other;

Gaps ö Length 24; Indels Score 17.2; DB 1; Pred. No. 2.4e+02; 0; Mismatches 3; 0, 1.6%; 86.4%; Conservative Local Similarity tes 19; Conserv Query Match Matches

; 0

à

RT-PCR primer of the invention SEQ ID 11. ACTACTAAAAATACAAAAAA 1 370/c AAX18370 standard; DNA; 17 (first entry) 11-MAY-1999 RESULT 24 g

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss. 97JP-0208312, JP11032765-A 09-FEB-1999 Synthetic

97JP-0208312.

18-JUL-1997;

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(TAKI ) TAKARA SHUZO CO LTD
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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where x = alabelled compound and/or a nucleotide with voluntary sequence; of alpha; beta, delta = thymine; n = natural number indicating the repetition of alpha; beta, delta = to N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for reproductive and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.
                                                                                                     Peptides having at least two new nucleotides
RT-PCR
                                                                                                                                                                                                                                                Disclosure; Page 11; 19pp; Japanese.
WPI; 1999-183822/16.
```

- useful as primers in

Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;

Query Match
1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; 1082 TTAAAAAAAAAAA 1098 17 TTAAAAAAAAAAAA à

AAA98232 standard; DNA; 17 RESULT 241 AAA98232/c

AAA98232;

30-JAN-2001 (first entry)

Human retrovirus HERV LTR PCR primer #31. Cell-specific expression; U3-R segment; Lo

expression; tissue-specific expression; gene therapy; ITR; long terminal repeat; retroviral expression vector;

Human retrovirus. WO200053789-A2. 14-SEP-2000 09-MAR-2000; 2000WO-EP02064. 10-MAR-1999; (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT

& GESUNDHEI.

Baust C; Leib-Moesch C, Schoen U,

WPI; 2000-587442/55.

This invention describes a novel retroviral expression vector (A) containing DNA sequences (I) for packaging vector RNA and for cell-specific expression of proteins or peptides encoding by heterologous DNA (II). The sequences controlling cell-specific expression contain a Retroviral expression vector, useful in gene therapy, contains a promoter from a human endogenous retrovirus to provide cell-specific Disclosure; Page 27; 67pp; German.

CC cell-specifically regulatable promoter region (P) from a human endogenous retrovirus (HBRV) DNA sequence. The invention also describes (a) mRNA and cell (A); (b) prokaryotic and eukaryotic cells containing (A); (c) and containing a retroviral expression vector RNA derived from (A); (e) a method for producing the virions of (d); (f) a method for incorporating containing a retroviral expression vector RNA derived from (A); (e) a method for producing the virions of (d); and (g) a retroviral vector system infection with the virions of (d); and (g) a retroviral vector system containing (A) and a packaging cell line, that contains at least one proteins of (A). (A) are used for cell- or tissue-specific expression of cereominant) retrovirus construct that encodes for the packaging for introducing or proteins of (A). (A) are used for cell- or tissue-specific expression of (I) into the enromesomal DNA of eukaryotic cells, preferably mammalian consorted for encomesomal DNA of eukaryotic cells, preferably mammalian consorted such as equired for transcription in a consorted such consorted for transcription in a consorted such and limited cell specificity). Since (A) are derived from endogenous (harmless) viral sequences, they do not introduce any new types of retrovirus. The promoters provide cell or tissue specific 8888888888888888888888888888888888

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;

1.5%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.(Matches 17, Conservative

Gaps

. 0

à g

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Gaps

· 0

Length 17; 0; Indels

AAA50197 standard; DNA; 17 BP. RESULT 242 AAA50197,

AAA50197;

(first entry) 07-NOV-2000

2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.

Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.

Synthetic.

/*tag= a /note= "2'-methoxyethoxy modified thymidine" Location/Qualifiers Key modified_base modified_base

*tag= b /note= "phosphorothioate internucleoside linkages"

WO200047593-A1.

17-AUG-2000.

11-FEB-2000; 2000WO-US03543.

99US-0250075

12-FEB-1999;

(ISIS-) ISIS PHARM INC

Manoharan M,

WPI; 2000-558188/51,

Preparation of mixed backbone cligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages

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The present sequence is that of a phosphorothicate oligonuclectide containing 20 T nucleobases, each having a 2' methoxyethoxy group on its 5' ribbayl sugar moiety. It is an example of an oligomeric compound produced according to the methods of the invention. The mixed backbone oligomeric, or chimeric, compounds having phosphorothicate and/or phosphoramidate internucleoside linkages in addition to phosphorothicate and/or phosphoramidate internucleoside linkages. The methods utilise H-phosphorate internucleoside linkages. The methods utilise H-phosphorate internucleoside linkages. The methods utilise H-phosphorate internucleoside linkages. Bach internucleoside linkages prior to further elongation. Mixed contiguous regions is subsequently oxidized to phosphodiseter, internucleoside linkages prior to further elongation. Mixed contiguous regions is subsequently oxidized to phosphodiseter, internucleoside linkages prior to further elongation. Mixed backbone oligomeric compounds are prepared in this manner by compounds of the invention are prepared using novel oxidation steps chat oxidized a region of 1 or more H-phosphonate internucleoside had oxidized. The oligomucleotides obtained are useful as primers in PCR, probes, linkages that have been primers in PCR, probes, linkers, gene fragments and for other primers in PCR, probes, linkers, gene fragments and for other cresarch reagents, and as antiviral agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;
Example 12; Page 34; 49pp; English.
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1.5%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 1.8e+02; 0; Indels Query Match
1.5%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 17; Conservative 0; Mismatches 1084 AAAAAAAAAAAAA 1100 17 AAAAAAAAAAAA 1 õ

AAA25450 standard; DNA; 17 BP. 19-JUL-2000 AAA25450; RESULT 243 AAA25450/c

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948. (first entry)

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; attisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

WO9954459-A2 Homo sapiens

28-OCT-1999

99WO-US08547. 19-APR-1999;

98US-0103636 98US-0082404 20-APR-1998; 23-JUN-1998;

(RIBO-) RIBOZYME PHARM INC.

Bellon L; Karpeisky A, Haeberli P; Beigelman L, McSwiggen JA, Zwick M, Jarvis T, Woolf T, Matulic-Adamic J; Thompson JD, Reynolds M,

WPI; 2000-013248/01.

New nucleic acids that interact, and optionally cleave, target

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with a target sequence and contain at least one phosphoro(di)thicate with a target sequence and contain at least one phosphoro(di)thicate.

C atalytic nuclest caid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or reated cells, or for other conditions associated with levels of can also be used to correlate inhibition of gene expression with carried as research reagents (for RNA, in the same way that respects, and as research reagents (for RNA, in the same way that carried and or attricularly for identification of therapeutic restriction endonucleases are used with DNA). The combination of carresponding target sequences, and AAA24748 to AAA2592 represent their corresponding target sequences, and AAA24748 to AAA2592 represent their receptor hairpin ribozyme sequences, and AAA26107 to AAA2618 represent their corresponding target sequences. AAA2593 to AAA26107 to AAA2618 represent their checkport hairpin ribozyme sequences. AAA25219 to AAA2611 represent corresponding target sequences. AAA25219 to AAA2611 represent corresponding target sequences. AAA26219 to AAA26211 represent corresponding target sequences. AAA25219 to AAA26211 represent corresponding target sequences. AAA26219 to AAA26211 represent corresponding target sequences. AAA26219 to AAA26211 represent corresponding target sequences. AAA26219 to AAA26211 represent corresponding target sequences and antisense oligonucleotides used in the corresponding target invention.
                                                                                                                                      present invention describes nucleic acids (A) that interact stably
                                                                   Claim 77; Page 79; 148pp; English.
sequences, used to treat cancer
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/ Match
Local Similarity 100.0%; Pred. No. 1.8e+02;
les 17; Conservative 0; Mismatches 0; Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other; 1084 AAAAAAAAAAAAAA 1100 Query Match Matches ð

17 AAAAAAAAAAAAA 1

Db

6

Gaps

0;

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Gaps . 0

Length 17; Indels

> AAQ34110 standard; DNA; 18 (updated)
> (first entry) 25-MAR-2003 02-FEB-1993 AAQ34110; RESULT 244 AAQ34110

Sequence of a microsatellite from clone TGLA60B.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus.

WO9213102-A1 06-AUG-1992, 92WO-US00340. 91US-0642342. 15-JAN-1992; 15-JAN-1991;

Georges M, Massey JM; WPI; 1992-284684/34. (GENM-) GENMARK.

- used in genetic identification, gene mapping, and selective breeding Table 7; Page 375; 517pp; English. Polymorphic bovine DNA markers

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between

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Ma.
Local S...
17;
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                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                            RESULT 246
                                                                                                                                                                                                                                                                                        AAT94668/c
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               888888888888888
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250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

Come out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MooI sites, the frequency of
(TG)n >9 microsatellites in the bovine genome is estimated at >100,

COO. The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence
amplification of the corresp. microsatellite (using the program
oPTIPRIM). The microsatellites may be used to identify individuals,
for parentage testing, and in the genetic mapping of economic trait
cori, or genes involved the determinism of economically important
traits esp. in cattle, to allow selective breeding.

Cupdated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo, removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect Abs, in which case the ligand is an oligo-labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary olgi is AAQ75024 which can be covalently attached by the 5'-terminus to the N- or C-terminal of a synthetic peptide. In the example, peptide AAR62941 was coupled to oligo AAQ75024 using
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection
                                                                                                                                                                                                                           1.5%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                  Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic oligo; solid phase immunoassay; ss.
                                                                                                                                                                                                                                     100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example, Page 12; 34pp; English.
                                                                                                                                                                                                                                                                                                   1 AAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0061694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US05407
                                                                                                                                                                                                                                                                                                                                                              AAQ75025 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-006819/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9426932-AI
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03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                      AAQ75025;
                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                        RESULT 245
AAQ75025/c
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disuccinimidyl suberate. Serum samples suspected to contain HEV Abs were immobilised on plastic tubes or wells, then incubated for 30-60 onins with the peptide-oligo proruct. The vessels were washed; bound oligo was released with 0.2M glycine and amplified in a separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR. The glycoslase to remove the U18 fragment, and the product captured by immobilised oligo-dT.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in
                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant; snapdragon; primer; ss.
                                                                                                                                                                                                                                                                                                                                  1.5%; Score 17; DB 1; Le
.00.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    manipulate the pigmentation of transgenic plants.
                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                         Sequence 18 BP; 0 A; 0 C; 0 G; 18 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anchored poly(T) oligonucleotide polyT-AnchC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael MZ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Page 59; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT94668 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brugliera F, Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FLOR-) FLORIGENE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-448691/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT94668;
                                                                                                                                                                                                                                                                                                                               Query Match
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Gaps

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1.5%; Score 17; DB 1; Length 18; Similarity 100.0%; Pred. No. 1.9e+02; 17; Conservative 0; Mismatches 0; Indels

1084 AAAAAAAAAAAAA 1100

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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "phosphorothioate internucleotide linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorothioate; electrospray ionisation-Fourier transform; mass spectrometry; off-resonance excitation; ss.
                                                                                                                                                                                                                                Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorothioate oligodeoxynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                           Example 1; Page 47; 70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1082 TTAAAAAAAAAAAA 1098
                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                       98WO-JP00905.
                                                                                                                    97JP-0050302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0040717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV07750 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US04919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TTABABABABABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                      WPI; 1998-495844/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                             WO9839437-A1.
                                                                                     05-MAR-1998;
                                                                                                                05-MAR-1997;
                                                        11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1998.
Synthetic.
                                                                                                                                                                         Sakaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV07750;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAV07750
à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream region of a polyadenylation sequence. They were used to prime cDNA sythesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and were also utilised in the PCR amplification of plant cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding flavonoid 3' hydroxylase (see AAM35704) was isolated using a differential display approach. This can be used to manipulate the pigmentation of transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                     Flavonoid 3' hydroxylase; pigmentation; flower colour;
transgenic plant; snapdragon; primer; ss.
                                                                                                                                                        Anchored poly(T) oligonucleotide polyT-AnchG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Michael MZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Page 59; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1084 AAAAAAAAAAAAA 1100
                                                                    AAT94669 standard; DNA; 18 BP.
 AAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                          97WO-AU00124
                                                                                                                                                                                                                                                                                                                                                      96AU-0008386
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                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                               (FLOR-) FLORIGENE LID
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-448691/41
                                                                                                                              27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                           Brugliera F,
                                                                                                                                                                                                                                                                                                                       28-FEB-1997;
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                                                                                                                                                                                                                                                               WO9732023-A1
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                                                                                                                                                                                                                                   Synthetic.
 17
                                                                                                    AAT94669;
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                                          RESULT 247
                                                          AAT94669,
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0

Gaps

0

BP.

(HYBR-) HYBRIDON INC

Wang BH;

PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.

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WPI; 1998-520830/44.

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The invention relates to an analytical method for determining the mucleotide sequence of nucleic acid analytes, including chemically modified oligonucleotides. This new method utilises electrospray instainon-Fourier transform mass spectrometry. The ions are excited by sustained off-resonance excitation with single shot excitation, and the target fragmented by collisionally activated dissociation by a neutral gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation of biology and biomedical application. The method is used in molecular biology and biomedical applications. The method is used in molecular constance transform ion cyclotron resonance mass spectrometry, is extremely rapid and acts directly on the oligonucleotide. The method is effective for a variety of nucleic acid analytes, particularly chemically modified oligonucleotides which have not previously been successfully sequenced. The present sequence represents a
                    sequence of a nucleic acid analyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 other;
                                                                                                                                           Example 1; Figure 3A; 25pp; English.
                                                              using electro-spray ionisation
Determining the nucleotide
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Gaps ; 0 Length 18; / Match 1.5%; Score 17; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 1.9e+02; nes 17; Conservative 0; Mismatches 0; Indels Query Match Best Local S Matches ð

g

RESULT 250 AAV37712

AAV37712 standard; cDNA; 18 BP. (updated)
(first entry) 25-MAR-2003 07-SEP-1998 AAV37712;

Human protein AQ2_1i 3'-portion and polyA tail.

Human; secreted protein; murine adult spleen; human foetal kidney; ovary; bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; L256_1i; prevent; treat; amelforate; medical; ds.

Homo sapiens

WO9820130-A2

14-MAY-1998.

97WO-US19857. 31-OCT-1997;

96US-0742973. 01-NOV-1996; 29-OCT-1997;

(GEMY) GENETICS INST INC.

Merberg McCoy JM, Lavallie ER, Treacy M; Jacobs K, aulding V, Spaulding WPI; 1998-286946/25. Agostino MJ, Racie LA,

New secreted proteins and associated polynucleotides - obtained from murine adult spleen, human foetal kidney, human ovary, murine bone marrow and murine adult thymus

Disclosure; Page 58; 75pp; English.

The present invention describes novel proteins isolated from cDNA clones: AE648_11; AE693_11; AK438_11; AK609_11; AM1060_11; AQ2_11;

K433_11; or L256_11, deposited as ATCC 98237. The present sequence represents the 37-portion of AQ2_11 isolated from a human ovary cDNA library. The proteins from the present invention may be administered in a composition to prevent, treat or ameliorate a medical condition. The proteins may exhibit biological activities such as nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis regulating chemotactic/chemokinetic activity, haematopoiesis regulating chemotactic/chemokinetic activity, haematopoiesis and thrombotic activity, receptor/ligand activity, humbition activity, receptor/ligand activity, tumour inhibition activity, and other

Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;

(Updated on 25-MAR-2003 to correct PR field.)

.; 0 1.5%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels Query Match 1.5 Best Local Similarity 100. Matches 17, Conservative

0;

Gaps

δ ΩĐ RESULT 251 AAV21970/c

; 0

BP. AAV21970 standard; DNA; 18

AAV21970;

14-JUL-1998 (first entry)

Nuclease resistant antisense oligo NBT 13 targeted against (T)18.

Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; ss.

Synthetic.

WO9803533-A1.

29-JAN-1998.

97WO-US12961 23-JUL-1997;

96US-0685575 24-JUL-1996;

(OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.

Thompson TL; Arrow A, Dale RMK,

WPI; 1998-120687/11.

Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s) with antibiotics

Claim 49; Page 87; 163pp; English.

This antisense oligonucleotide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant oligonucleotides, targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease resistant oligonucleotide can be covalently linked to an antibiotic. The method is used to treat infections by a wide variety of Gram-positive and Gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in immuno-compromised individuals (e.g. patients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or

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AAX19943/c
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fused to, antiviral or other antimicrobial oligonucleotides. Apart from therapeutic use, the oligonucleotides can be used to control bacteria in laboratory cultures, foods, beverages and industrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism in mammalian cells. They may also activate RNase H and have a general, non-specific immune-stimulating effect. The oligonucleotides can be administered orally, intransally, rectally, topically or by injection, optionally coupled to an agent (e.g. carbohydrate or polyamine) that enhances cellular uptake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed for labelling an oligonucleotide having a adenine and thymine or uxacil or guanine and vivosine, and n is an integer of lor more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA. polymerase lacked in 5' to The method can detect a gene in a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used than prior art methods. The present sequence represents a primer used
                                                                                                                                                                                                                                                                                                                                                                                                   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
                                                                                                                                                                                       Gaps
                                                                                                                                                                                     ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes
                                                                                                                                                 DB 1; Lens.
3. 1.90+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Labelling of an oligonucleotide - useful for detecting
                                                                                                                              Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                        1.5%; Score 17; DB 100.0%; Pred. No. 1.9 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                           Primer SEQ ID NO:2 from JP11075880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 7; 10pp; Japanese.
                                                                                                                                                                                                           1084 AAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0195719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0205378
                                                                                                                                                                                                                               18 AAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                               AAX19942 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                     Local Similarity 100.
18 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-257710/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP11075880-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                 14-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                         AAX19942;
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Matches
                                                                                                                                                                                                                                                                       RESULT 252
                                                                                                                                                                                                                                                                                    AAX19942
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A method has been developed for labelling an oligonucleotide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a gene. The method can detect a gene in a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labelling of an oligonucleotide - useful for detecting genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 1.5%; Score 17; DB 1; Le
Local Similarity 100.0%; Pred. No. 1.9e+02;
Nes 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT-PCR primer of the invention SEQ ID 14.
                                                                                                                          Primer SEQ ID NO:3 from JP11075880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 7; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                 98JP-0195719
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AAX19943 standard; DNA; 18
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX18373 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-257710/22.
                                                                                                                                                                                                                                                JP11075880-A.
                                                                                                                                                                                                                                                                                                                                 10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                        14-JUL-1997;
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                                                                                 14-JUN-1999
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                                                                                                                                                                                                         Synthetic.
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                                        AAX19943;
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Matches
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Gaps

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Best Local Similarity Matches 17; Conserv

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The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperricemia and sleep apnea syndrome. The genes (AAZ20631-633) and the proteins (AAZ5059-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
           This invention describes novel secreted human proteins (I) which have cytostatic, immunostimulatory, antimicrobial, antiviral, immunostimulatory, antimicrobial, antiviral, immunosuppressive, antiminflammatory and vulnerary activity and which at as cytokine, cell proliferation or differentiation regulators. (I) is useful for treating tumors, autoimmune diseases, inflammatory disorders, wounds, microbial infections and viral diseases. (I) is also useful for suppressing graft versus host reaction. AAA40490-A40580 represent cDNA fragments that encode the secreted proteins AAB10226-B10288 described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   physiologically active protein specifically derived from mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5%; Score 17; DB 1; Length 18; 0.0%; Pred. No. 1.9e+02; 0. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adipose tissue gene amplifying primer #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                         Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5°,
100.08; Pic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ90646 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-2000
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                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 256
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X888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                    This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula:

(X) m5. (alpha)n-beta-N3. or (X) m5. (gammalk-delta-N3.; where
X = a labelled compound and/or a nucleotide with voluntary sequence;
m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
A alpha; bera, delta = v or Ni, v = adenine, gamma = thymine or cytosine;
N = adenine, quanine, cytosine or thymine; gamma = thymine;
k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for FT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors, autoimmune diseases, inflammatory disorders, wounds, microbial infections and viral diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; cytostatic; immunostimulatory; antimicrobial; antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine; cell proliferation; differentiation; regulator; treatment; tumor; autoimmune disease; inflammatory disorder; wound; microbial infection; viral disease; graft versus host reaction suppression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                     - useful as primers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 1; Length 10;
Pred. No. 1.96+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 other;
                                                                                                Peptides having at least two new nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adult ovary cDNA fragment AQ2_1i #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 269; 293pp; English.
                                                                                                                                                                   Disclosure; Page 11; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LaVallie ER,
Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Sco...
100.0%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA40563 standard; cDNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US31005.
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             (TAKI ) TAKARA SHUZO CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 17; Conservative
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-442661/38.
P-PSDB; AAB10274.
                                                       WPI; 1999-183822/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1999;
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Merberg D,
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Gaps

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The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises eligonuclectides centablings expaints that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
belix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonuclectides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
expression or to prevent DNA replication, or reverse transcription of
inhibit retroviruses. The compositions are therefore particularly used to
inhibit retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonuclectides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonuclectides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins They target ss
RNA, but not complementary ss DNA, so may be useful for targeting
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonuclectides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
commal oligomuclectides containing beta-D-arabinose used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication
                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "Ribose moiety replaced by beta-D-arabinose"
                                                                                                                                                                                                   Beta-D-arabinose, antisense, inhibition,
transcription, expression, reverse transcription,
viral replication, RNase H cleavage, triple helix formation, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noronha AM, Wilds C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                             Oligoarabinonucleotide SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 29; 91pp; English.
                                        AAZ87161 standard; RNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-CA00571.
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                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMC-) UNIV MCGILL.
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                                                                                                                                                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998;
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                                                                                                                        08-MAY-2000
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                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                AAZ87161;
RESULT 257
                       AAZ87161
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Borkow G,

Gaps .; Query Match 1.5%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 17; Conservative 0; Mismatches 0; Indels 17; Conservative

0;

Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication /*tag= a /note= "Ribose moiety replaced by beta-D-arabinose" transcription; expression; reverse transcription; viral replication; RNase H cleavage; triple helix formation; ss. Arion Borkow G, Noronha AM, Wilds C, Beta-D-arabinose; antisense; inhibition; Location/Qualifiers Oligoarabinonucleotide SEQ ID NO:3. 1 AAAAAAAAAAAAAA 17 AAZ87162 standard; RNA; 18 BP 99WO-CA00571. 98CA-2241361. 08-MAY-2000 (first entry) Damha MJ, Parniak MA, WPI; 2000-160584/14. (UYMC-) UNIV MCGILL. Key modified_base 17-JUN-1999; 19-JUN-1998; WO9967378-A1 29-DEC-1999. Synthetic. AAZ87162; RESULT 258 AAZ87162/ g

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Example 1; Page 29; 91pp; English.

The invention relates to a new composition for selective; sequence—
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonuclectides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
helix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonuclectides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
RNA by retroviruses. The compositions are therefore particularly used to
inhibit retroviruse. The compositions are therefore particularly used to
inhibit retrovirus replication. The oligoarabinonuclectides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonuclectides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins. They target ss
RNA, but not complementary ss DNA, so may be useful for trargetting
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonuclectides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
normal oligonuclectides. Sequences AAZ87160-Z87164 represent
oligoarabinouclectides containing beta-D-arabinose used in an exemplification of the present invention.

Sequence 18 BP; 0 A; 0 C; 0 G; 18 U; 0 other;

Gaps . 0 Query Match 1.5%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 17; Conservative 0; Mismatches 0; Indels

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1084 AAAAAAAAAAAAA 1100

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The invention relates to a new composition for selective, sequence—
Specific inhibition of gene transcription and expression in a host. The composition comprises oligonucleotides containing arabinose sugars that can hybridise to either a single-stranded (ss) RNA to induce RNase H cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple helix, thereby inhibiting DNA replication and/or transcription. The oligoarabinonucleotides are used for antisense inhibition. The oligoarabinonucleotides are used for antisense inhibition of gene expression or to prevent DNA replication, or reverse transcription of mibit retroviruses. The compositions are therefore particularly used to inhibit retroviruses. The compositions are therefore particularly used to inhibit retrovirus a replication. The oligoarabinonucleotides can also be used, in combination with RNase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinonucleotides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target as the complementary as DNA, so may be useful for targetting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligonucleotides. Sequences AAZSH169 represent on a rabinose used in an exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
"Deoxyribose moiety replaced by 2'-deoxy-2'-
fluoro-beta-D-arabinose"
                                                                                                                                                                                                                                                                                        2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription;
viral replication; RNase H cleavage; triple helix formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noronha AM, Wilds C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                       Deoxyarabinonucleotide SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 31; 91pp; English.
1084 AAAAAAAAAAAAA 1100
                                                                                                                                    AAZ87166 standard; DNA; 18 BP.
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Damha MJ, Parniak MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-160584/14.
                                                                                                                                                                                                                                                                                                                                                                                                                Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                           AAZ87166;
                                     18
                                                                                                                 AAZ87166/
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Arion D;

Borkow G,

1.5%; Score 17; DB 1; Length 18;

Query Match

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The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The composition comprises oligonuclecties containing arabinose sugars that can hybridise to either a single-stranded (ss) RNA to induce RNase H cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple helix, thereby inhibiting DNA replication and/or transcription. The oligoarabinonucleotides are used for antisense inhibition of gene expression or to prevent DNA replication, or reverse transcription of RNA, by retroviruses. The compositions are therefore particularly used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibit retroviral replication. The oligoarabinouncleotides can also be used, in combination with RNase H, as reagents for sequence-specific claravage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinonucleotides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target ss RNA, but not complementary as DNA, so may be useful for targetting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligouncleotides. Sequences AA287165-287169 represent containing 2'-deoxy-2'fluoro-beta-D-arabinose used in an exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arion D;
                                                                                                                                                                                                                                                                                                                                                            transcription; expression; reverse transcription;
viral replication; RNase H cleavage; triple helix formation; ss.
                                 ·
0
                                                                                                                                                                                                                                                                                                                                         2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borkow G,
                                 Indels
                Pred. No. 1.9e+02; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluoro-beta-D-arabinose"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Noronha AM, Wilds C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Deoxyarabinonucleotide SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 31; 91pp; English.
100.0%; FI:
                                                                     1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                              AAZ87167 standard; DNA; 18 BP.
                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-CA00571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98CA-2241361
                                                                                                       (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parniak MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-160584/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMC-) UNIV MCGILL.
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1998;
                                                                                                                                                                                                                                                                   08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9967378-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1999.
                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Damha MJ,
                                                                                                                                                                                                                                   AAZ87167;
                                                                                                                                                            RESULT 260
                                     Matches
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Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant; nephrotropic; antiinflammatory; gene therapy; cardiac disease; renal disease; inflammatory disease; polylinker; ss.

27-SEP-2000; 2000WO-US26582.

WO200123419-A2.

Synthetic,

05-APR-2001.

99US-0156277

27-SEP-1999;

(SCIO-) SCIOS INC.

Phagemid vector pCR2.1 polylinker oligonucleotide #6.

(first entry)

29-JUN-2001

AAF82472;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to methods and kits for amplification of mRNA using a primer in PCR that contains an RNA polymerase (RNAP) promoter. The invention provides methods for amplification and detection of RNA derived from a population of cells, preferably eukaryotic cells and most preferably mammalian cells, which methods preserve fidelity and most preferably mammalian cells, which methods preserve fidelity with anable amplification of extremely small amounts of mRNA. The method and kit are useful for amplifying and detecting RNA derived from a population of cells, especially eukaryotic cells like mammals. The RNAs generated are useful for profiling gene expression in different populations of cells. The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro transcription) method of the invention.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                    RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amplifying and detecting RNA derived from a population of cells by employing a primer that contains an RNA polymerase promoter in a polymerase chain reaction -
                                                                             0;
                                                                                                                                                                                                                                                                                                                                  mRNA fragment used in 3' end PCR/IVT method of the invention.
                                 Query Match
1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 17 A; 0 C; 0 G; 0 U; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROSE-) ROSETTA INPHARMATICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1; 29pp; English.
                                                                                                        1084 AAAAAAAAAAAA 1100
                                                                                                                                                                                                                            AAD20091 standard; mRNA; 18 BF.
                                                                                                                                        1 AAAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0411074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0411074
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schelter JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-624273/72.
                                                                                                                                                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          US6271002-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linsley PS,
                                                                                                                                                                                                                                                               AAD20091;
                                                                                                                                                                                           RESULT 261
                                                                                                                                                                                                               AAD20091
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The present sequence corresponds to polylinker DNA of the phagemid vector pCR2.1. It was used in the construction of a normalised rat CDNA library, which was used in an example demonstrating differential expression of a rat gene referred to as clone P00210D09. The invention clates to a polypeptide comprising a sequence of at least 80% identity to residues 22-122 of the present sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one polypeptides and polymospide encoded by clone P00210D09. The polypeptides and polymospide encoded by clone P00210D09. The polypeptides and polymospide of the invention are useful for the polymospides are useful in antisense mediated gene inhibition and in gene therapy. The polypeptides are useful in assays for identifying lead compliant may be used as therapoutic agents in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarrhythmic; antiarteriosclerotic; antiarherosclerotic; nephropathic; antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid; antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel secreted factor encoded by clone P00210D09 useful for diagnosing, treating and/or preventing various cardiac, renal and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac, kidney or inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 41; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD03565 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                               Stanton LW, Kapoun AM;
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-328177/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
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Gaps

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0; Indels

1.5%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.9e+02; iive 0; Mismatches 0; Indels

1084 AAAAAAAAAAAAA 1100

Local Similarity 100. Les 17; Conservative

Matches

à

Query Match

ААААААААААААА 18

AAF82472 standard; DNA; 18 BP.

RESULT 262
AAF82472/c
ID AAF8247
XX

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nootropic; neuroprotective; congestive heart failure; myocarditis; hypertropic cardiomyopathy; angina pectoris; myocardial infarction; kidney disease; acute renal failure; renal glucosuria; renal infarction; polycystic kidney disease; hereditary nephritis; inflammatory disease; stroke; neurour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis; stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis; ulcerative colitis; Alzheimer's disease; gene therapy; ss.
                                                                                                                                 27-SEP-2000; 2000WO-US26544
                                                                                                                                                                                         Stanton LW, Kapoun AM;
                                                                                                                                                                                                           WPI; 2001-266159/27
                                                                                                                                                                      (SCIO-) SCIOS INC.
                                                                         Rattus norvegicus
                                                                                           WO200123564-A1
                                                                                                                                                  27-SEP-1999;
                                                                                                              05-APR-2001
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99US-0156280

The patent discloses novel secreted factor protein encoded by clone pounds D12. The secreted factor is differentially expressed in certain discase states. Secreted protein, its antibodies, antagonists or compositions comprising them are useful in the diagnosis and treatment of cardiac diseases such as congestive heart failure, myocardial infeation, cardiac arrhythmia, arteriosclerosis, myocardial infarction, cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal failure, renal glucosuria, renal infarction, nephroganic diabetes inspipulas, polyoyatic kidney disease, hereditary nephritis and inflammatory diseases such as sethma, autoimmune diabetes, tumour angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndome, sathma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis, Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted protein DNA is useful in antisense-mediated gene inhibition and gene therapy. An array comprisaing one or more oligonucleotides complementary to reference RNA or DNA encoding the secreted factor is useful for detecting cardiac, kidney and inflammatory disease. The normalised cDNA library containing secreted factor buns. The normalised cDNA library containing secreted factor DNAs. The normalised cDNA library containing secreted factor of differentially expressed rat secreted factor P0188_D12 gene. Novel secreted factor encoded by clone P00188D12 which is differentially expressed in certain disease states, useful in diagnosing and treating cardiac, renal or inflammatory diseases Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other; Example 1; Page 42; 71pp; English.

Gaps ; Length 18; Indels th 1.5%; Score 17; DB 1; Le Similarity 100.0%; Pred. No. 1.9e+02; 17; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 17; Conserv à

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AAF99708 standard; DNA; 18 AAF99708; AAF99708/c
ID AAF99
XX
AC AAF99
XX
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XX
DT 12-JU
XX
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XX
XX
XX RESULT

(first entry) 12-JUN-2001

Immunostimulatory nucleic acid #824.

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. toxoplasma, retroviridae, and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a lact to a Th1 immune response and to activate immune cells.

Note: the present sequence may have a phosphorothioate backbone.
    anti-parasitic;
                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids -
Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-par
immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; passitic infection; cancer; asthma;
infectious disease; allergy; immune deficiency; phospborothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                                 25-SEP-1999; 99US-0156113.
27-SEP-1999; 99US-0156135.
23-AUG-2000; 2000US-0227436.
                                                                                                                                                                                                                          25-SEP-2000; 2000WO-US26383.
                                                                                                                                                                                                                                                                                                                                                (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                      (COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                            Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-273485/28.
                                                                                                                                           WO200122972-A2
                                                                                                                                                                                 05-APR-2001
                                                                                                  Synthetia.
                                                                                                                                                                                                                                                                                                                                                                                                            Krieg AM,
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Gaps ; 0 Length 18; 0; Indels 1 1.5%; Score 17; DB 1; Le Similarity 100.0%; Pred. No. 1.9e+02; 17; Conservative 0; Mismatches 0; 17; Query Match Best Local (Matches

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

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1084 AAAAAAAAAAAAA 1100 ~ 18 АААААААААААААА

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Immunostimulatory nucleic acid #850. (first entry) 12-JUN-2001

BP

AAF99734/c ID AAF99734 standard; DNA; 18

RESULT 265

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AAF99734;

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; . 83 infectious disease; allergy; immune deficiency; phosphorothioate; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma;

Synthetic.

WO200122972-A2

us09904568-1.rng

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th1 immune response and to activate immune cells.
                                                                                                                                                                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory \mathrm{Py}\text{-}\mathrm{rich} and TG nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scaffold protein; antibody mimic, fibronectin type III domain; randomised loop; randomised beta-sheet; diagnostic purpose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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/note= "Linked to (PEG)2CCPuromycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                    Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide A18-2PEG linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AAAAAAAAAAAAA 2
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                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
                                          25-SEP-2000; 2000WO-US26383
                                                                                                                                   23-AUG-2000; 2000US-0227436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD17014 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                 Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             randomised loop; rando
protein designing; ss.
                                                                                                                                                                                                                                                                                            WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200164942-A1
                                                                                      25-SEP-1999;
27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc feature
05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001
                                                                                                                                                                                                                                                 Krieg AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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mimics)
                                                                                                                                                                                                                                                           The present invention relates to an array of proteins (antibody mimics comprising a fibronectin type III domain having a randomised loop, a randomised beta-sheet, or their combination, and has the capacity to bind to a compound that is not bound by a corresponding naturally-occurring fibronectin, immobilised onto a solid support. The antibody mimics is useful for detecting a compound preferably a protein, in a biological sample. It is also useful to detect one or more different analytes simultaneously in a sample. Hence is useful for diagnostic purposes. It is also useful for the purpose of designing proteins capable of binding to virtually any compound of interest. The present sequence is an oligonucleotide Al8-2PEG linker used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiogenesis inhibitor; ss, angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                          Fibronectin scaffold protein array for obtaining a protein/compound which binds to a compound/protein, comprises a fibronectin type III domain having a randomized loop, a randomized beta-sheet or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 1; Ler
; Pred. No. 1.9e+02;
----hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiogenesis inhibitory oligonucleotide #913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prea. ...
                                                                                Kuimelis RG;
                                                                                                                                                                                                                                 Disclosure; Page 25; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 AAAAAAAAAAAAA 1100
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             29-FEB-2000; 2000US-0515260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS78429 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                Wagner RW,
                                                                                                               WPI; 2001-557782/62.
                                             (PHYL-) PHYLOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bratzler RL;
                                                                              Lipovsek D,
                                                                                                                                                                                                 combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS78429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Thu Jan

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metaetasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, necolar degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Oaler-Webber Syndrome, mycoardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclarosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention.
                                                                                             Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                       Claim 2; Page 35; 276pp;
WPI; 2002-566690/60.
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Score 17; DB 1; Length 16; Pred. No. 1.98+02; Oriented 0; Indels Query Match 1.5%; Soc Best Local Similarity 100.0%; P Matches 17; Conservative 0; 1084 AAAAAAAAAAAAA 1100

AAAAAAAAAAAAAA 18 à 원

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ABS78455 standard; DNA; 18 RESULT 268 ABS78455/c

Angiogenesis inhibitory oligonucleotide #939. (first entry) 13-DEC-2002

Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

Synthetic.

40200253141-A2.

14-DEC-2001; 2001WO-US48458. 11-JUL-2002

14-DEC-2000; 2000US-255534P.

(COLE-) COLEY PHARM GROUP INC

3ratzler RL;

WPI; 2002-566690/60.

Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject

Claim 2; Page 36; 276pp; English

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tunnour growth, tunnour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasis, rubeosis, osler-Webber Syndrom, myocardial angiogenesis, plaque neovascularisation, telangiectasia, heemophiliac pints, angiofibrom, wound granulation, intestinal adhesions,
                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antianglogenic nucleic acid of the invention.
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Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Gaps ; 1.5%; Score 17; DB 1; Length 18; 00.0%; Pred. No. 1.9e+02; 0; Indels 100.0%; Pred. No. 1.> tive 0; Mismatches 17; Conservative Best Local Similarity Query Match Matches

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ABS53437 standard; DNA; 18 269 ABS53437/c

Gaps

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ABS53437;

BP.

(first entry) 29-NOV-2002

TC; ss; second strand cDNA synthesis; Terminal continuation; primer; poly d(T). Poly d(T) primer.

Synthetic.

WO200265093-A2

22-AUG-2002

14-FEB-2002; 2002WO-US05713.

14-FEB-2001; 2001US-268645P. 14-FEB-2001; 2001US-266664P. 18-UUL-2001; 2001US-306216P. 07-NOV-2001; 2001US-344557P. 07-NOV-2001; 2001US-344557P.

RES FOUND MENTAL HYGIENE INC. (BAYU) BAYLOR COLLEGE MEDICINE. (REME-)

Che S; Ginsberg SD, WPI; 2002-567050/60.

Increasing efficiency of second strand cDNA synthesis using terminal continuation model before performing further RNA amplification by RNA transcription

Example 7; Page 80; 128pp; English.

This invention relates to a novel method for increasing the efficiency of second strand cDNA synthesis through a mechanism of terminal continuation. In the method an RNA molecule is obtained and a first primer is added that comprises a region that hybridises to a complementary region of the molecule before a second primer is added comprising at least one riboguanine at the 3' end of the primer. A first

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complementary nucleic acid molecule is synthesised, the RNA molecule and second primer are removed and a second complementary nucleic acid molecule is synthesised to form a second hybrid with an extension product of the third primer bound to the first complementary molecule. The method of the invention is useful for increasing the efficiency of genetic signals from histologically stained tissue. The present expresents a poly d(T) PCR primer used in the method of the
                                                                                                                                                                                                         invention.
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Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

. 0 Score 17; DB 1; Length 18; Pred. No. 1.9e+02; 0; Indels 1.5%; Scot. 100.0%; Pred. No. 17; Conservative Query Match Best Local Similarity Matches ò

1084 AAAAAAAAAAAAA 1100 N 18 AAAAAAAAAAAAAA

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270

AAD41497 standard; DNA; 18 AAD41497;

BP

(first entry) 30-OCT-2002

Oligonucleotide used for amplifying sea hare cyplasin L DNA.

Apoptosis, ion channel modulator; hyperproliferative disease; tumour; therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma; Alzheimer, disease; parkinson's disease; arteriosclerosis; heart disease; stroke; vascular disease; nootropic; neuroprotective; cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.

Unidentified,

WO200231144-A2.

18-APR-2002.

12-OCT-2001; 2001WO-EP11837.

13-OCT-2000; 2000EP-0122466.

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN

Meyer TF; Rudel T, Machuy N, Butzke D,

WPI; 2002-537205/57.

Novel polypeptide having cytotoxic activity obtainable from Aplysia, useful for destroying tumors, for identifying novel targets for the development of anti-tumor agents, and as specific ion channel modulators

Example 5; Page 37; 87pp; English.

The present invention relates to novel polypeptides having cytotoxic activity obtainable from sea hare Aplysia. Sequences of the invention activity obtainable from sea hare Aplysia. Sequences of the invention resistant for the manufacture of cytotoxic agents against apoptosis-resistant cells, where the agents are useful for diagnosis, prevention, treatment of disorders associated with dysfunctions of GAP-SH3 binding protein, factors for generating or detoxifying reactive oxygen species (ROS) and factors for blocking and/or by-passing of caspases. They are useful for tumour therapy. Cytotoxic proteins of the invention are useful for tumour therapy. Cytotoxic proteins of the invention are useful for tumour therapy or selectively killing cells in tissues, for identifying novel targets for the development of pharmaceutical agents, preferably anti-tumour agents and as specific ion channel modulators, e.g., blockers or openers for therapy, diagnostic or research. They are useful for the diagnosis and therapy of hyperproliferative diseases,

preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma. They are also useful for development of drugs for the treatment of degenerative diseases such as Alzheimer's disease, Parkinson's disease, arteriosclerosis, heart diseases, stroke and vascular diseases. The present sequence is an oligomucleotide which is used for amplifying sea hare cyplasin L DNA. This sequence is used in the exemplification the invention.

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Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Gaps ; Length 18; Indels 1.5%; Score 17; DB 1; Le 100.0%; Pred. No. 1.9e+02; 100.0%; Pred. No. 1.3 Local Similarity 100. ses 17; Conservative Query Match Best Loca Matches

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1084 AAAAAAAAAAAAA 1100

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Gaps

18 AAAAAAAAAAAAAA 2

AAS94743 standard; DNA; 18 AAS94743,

AAS94743;

(first entry) 12-MAR-2002

Rat secreted factor DNA oligonucleotide probe #6.

Rat; secreted factor polypeptide, cardiac disease; renal disease; kidney; inflammatory disease; congestive heart failure; myocarditis; asthma; ss; dilated congestive cardionyopathy; angina pectoris; cardiac arrhythmia; myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke; atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome; renal infarction; hereditary nephritis; polycystic kidney disease; chronic renal failure; renal vehn thromboeis; medullary sponge kidney; rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer; graft versus host reaction; Crohn's disease; ulcerative colitis; probe; Alzheimer's disease; gene therapy.

Synthetic.

WO200174901-A2.

11-0CT-2001

23-MAR-2001; 2001WO-US09555

31-MAR-2000; 2000US-193548P.

14-MAR-2001; 2001US-0809545

(SCIO-) SCIOS INC.

Stanton LW, White

WPI; 2002-010779/01.

Novel secreted factor polypeptide useful for treating cardiac diseases such as arteriosclerosis, myocardial infarction, inflammatory diseases such as asthma, stroke, and rheumatoid arthritis and renal diseases

Example 1; Page 51; 189pp; English.

The invention relates to rat secreted factor polypeptides and the polynucleotides encoding them. The sequences are useful for treating cardiac, renal or inflammatory diseases. These include cardiac diseases such as congestive heart failure, myocarditis, dilated congestive cardiamyopathy, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and cardiac tumours, renal diseases such as glomerulonophritis, nephrotic syndrome, renal infarction, hereditary nephritis, polycystic kidney disease, chronic renal failure, renal vein thromboeis and medullary sponge kidney and inflammatory diseases such as asthma, rheumatoid

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Gaps

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Indels

100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0;

Best Local Similarity 100. Matches 17; Conservative

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Gaps . 0

Length 18;

0; Indels

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arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus host reaction, Crohn's disease, ulcerative colitis and Alzheimer's disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode the secreted factor polypeptides of the invention, and oligonucleotide
                                                                           1.5%; Score 17; DB 1; Le
100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                         Detection; comparative detection; adaptor; ss.
                                                         Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                      Adaptor oligonucleotide SEQ ID NO:2.
                                                                                                                1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                ABA93239 standard; DNA; 18 BP
                                                                                                                                  18 AAAAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                                                                                                  30-MAY-2000; 2000JP-0160324.
                                                                                                                                                                                                                     (first entry)
                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Comparative detection of
                                      probes and PCR primers.
                                                                                                                                                                                                                                                                                                                                                                       (UNIT-) UNITECH CO LID.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-135950/18.
                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                             JP2001333800-A.
                                                                                                                                                                                                                     18-APR-2002
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                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                   ABA93239;
                                                                           Query Match
                                                                                      Best Loca
Matches
                                                                                                                                                                        ABA93239/c
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The present invention describes a method for the comparative detection of the amount of an RNA. The method comprises: (a) CDNAs obtained by transcribing respectively from at least two tissue RNAs are respectively fragmented by using a same restriction enzyme; (b) each different adaptor and a common adaptor are added to each of the cDNA fragments derived from the same or different tissues by the step (a); (c) the resultant adaptoradded cDNAs are mixed together; (d) an adaptor primer having the common sequence to said different adaptor and a gene-specific adaptor are used to amplify said adaptor-added cDNAs containing no region derived from polyadenylic acid of the mRNA before the addition of the adaptor among the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the cONA amounts are measured between the tissues; (f) the RNA is detected from the measured result; (g) each different adaptor and a common adaptor are added to each of the genomic DNA fragments derived from a same or mind a common adaptor and a commo
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the amounts of RNA and DNA
                                                                                                                                                          Disclosure, Page 9; 9pp; Japanese.
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1084 AAAAAAAAAAAAA 1100

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Length 18;

DB 1;

1.5%; Score 17;

Query Match

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

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The present invention relates to methods for treating or preventing cancer, involving administrating to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, boan center, brain and central nervous system (CNS) cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, cancer, laukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, stomach cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, prostate cancer, and uterine cancer. The present sequence is an immunostimulatory oligonuclectide described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5%; Score 17; DB 1; Length 18; 0.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                         Immunostimulatory nucleic acid SEQ ID NO: 837,
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Best Local Similarity 100.0%; Pred. No. 1...
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                           angiogenesis; metastasis; cytostatic; ss.
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                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/*tag= a
/wod_base= OTHER
0;
                                   1084 AAAAAAAAAAAAA 1100
                                                                                                                                                     ABL39401 standard; DNA; 18 BP
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modified_base
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ABL39401/c
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BP.

(first entry)

04-AUG-1995

AAQ75555;

Analysis; gene

JP06303997-A

Synthetic.

01-NOV-1994

5555/c AAQ75555 standard; DNA; 19

RESULT 274

AAQ75555,

18 AAAAAAAAAAAAAA

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7578) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of
                                                                                                                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 other;
                                                                                                              TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restriction enzyme; ss.
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                    WPI; 1995-018287/03,
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                                  16-APR-1993;
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01-NOV-1994
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followed by
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restriction enzyme; ss.
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                                                                                                                                                                                                 Reverse transcription primer used in cDNA analysis technique.
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tive 0; Mismatches
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Page 5; 11pp; Japanese.

Disclosure;

WPI; 1995-018287/03.

93JP-0112515 93JP-0112515

16-APR-1993; 16-APR-1993; 1084 AAAAAAAAAAAAA 1100

à

Conservative

17;

Best Loca Matches

Local Similarity

Query Match

rapidly and easily.

AAAAAAAAAAAAA

17

RESULT 275

AAQ75557,

BP

AAQ75557 standard; DNA; 19

(first entry)

04-AUG-1995

AAQ75557

JP06303997-A.

aggregate;

Synthetic

Analysis;

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Gaps

RESULT 277

Matches

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8888888

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-scranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                              Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression; reverse transcription; primer; cDNA,
                                                                              Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 2e+02;
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100.0%; Pre
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AAQ75547/c
ID AAQ75547 standard; DNA; 19
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                                            04-AUG-1995
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                                                                                                                                                                   Synthetic.
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the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                     ch 1.5%; Score 17; DB 1; Length 19; l Similarity 100.0%; Pred. No. 2e+02; 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 1; Length 19;
Pred. No. 2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 other;
                                                                                        Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 other;
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100.0%; FL.
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                                                                                                                                                                                                                                                                                                                     BP.
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AAQ75550/c
ID AAQ75550 standard; DNA; 19 BP.
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Matches 17; Conservative
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                                                     rapidly and easily.
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by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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followed
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                                                                                                                         Query Match
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Gaps

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Length 19; 0; Indels

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cDNA and gene expression - by amplification of mRNA digestion with restriction enzymes
      WPI; 1995-018287/03
               Analysis of
followed by
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQVIS4T-07579) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 other;
Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rapidly and easily.
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; DB 1; Ler., o. 2e+02; o; Indels Mismatches Score 17; Pred. No. 1.5%; Scc_ 100.0%; Pred 0; 1 1084 AAAAAAAAAAAAA 1100 AAAAAAAAAAAAAA 1 17; Conservative Best Local Similarity 17 Matches à

Query Match

AAT10757 standard; RNA; 19 09-SEP-1996 AAT10757 RESULT

Electronically self-addressable device; ED; electrode; Oligonucleotide probe, T-2. (first entry)

current source; attachment layer; permeable; counterion; genetic typing; probe; detection; ss. Location/Qualifiers Synthetic.

Key modified_base

/*tag= /note= 25-JAN-1996

-amino terminus"

α į̇̃υ

94US-0271882 07-JUL-1994;

95WO-US08570

05-JUL-1995;

Heller MJ, (NANO-) NANOGEN INC. Evans GA,

Electronically self-addressable device - used for electronic control WPI; 1996-097582/10.

nucleic acid hybridisation

e.g.

Example 1; Page 61; 155pp; English.

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급

Sosnowski RG,

The sequences given in AAT10742-67 are synthetic oligonucleotides which are used in the construction of the electronically self-addressable device (ED) of the invention. The ED comprises a substrate, an electrode or opt. a number of electrodes supported by

the substrate, a current source operatively connected to the electrode and an attachment layer adjacent to the electrode which is permeable to a counterion but not permeable to a molecule capable of insulating or binding to the electrode. The attachment layer is capable of attaching a macromolecule. The ED is used for genetic typing and comprises a number of electronically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence. 888888888888888

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Gaps ö 1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity 17; Matches

0

1084 AAAAAAAAAAAAAA 1100 m 19 AAAAAAAAAAAAAA

g à

0

Gaps

, 0

BP AAV07878 standard; DNA; 19 (first entry) 14-DEC-1998 AAV07878;

phosphorothioate; ras gene; malignant cell growth; aminooxy-modified; nuclease resistance; reporter group; ss.

Aminooxy-modified oligonucleotide.

Synthetic.

/*tag= a /note= "5-methyl, 2'-aminooxyethoxy-thymidine" Location/Qualifiers /*tag= Key modified_base WO9835978-A1

98WO-US02405. 13-FEB-1998; 20-AUG-1998

98US-0016520 97US-0037143 30-JAN-1998; 14-FEB-1997;

(ISIS-) ISIS PHARM INC.

Cook PD, Kawasaki AM,

WPI; 1998-568232/48.

Manoharan M;

New aminooxy-modified oligonucleotides - which can show improved binding to complementary strands and improved resistance to nuclease

Disclosure; Page 84; 131pp; English.

The invention relates to aminooxy-modified(oligo)nucleotides or nucleosides which are useful as therapeutics, diagnostics, and research reagents. They may be used, e.g., for modulation of the ras gene and may be able to modulate the process of transformation from normal to malignant cell growth. They may be prepared using known methods. Inclusion of the aminooxy moieties can improve binding of oligonucleotides to complementary strands. The moieties can also provide conjugation sites useful for conjugation of useful ligands (e.g. reporter pharmacodynamic properties) to oligonucleotides. The present sequence represents an example of an aminooxy-modified oligonucleotide disclosed in the specification.

=

PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen; PSA; human; ss.

Homo sapiens. WO9932644-A2

PCR primer for PG1 biallelic marker 4-4-187.

(first entry)

27-SEP-1999

BP.

AAZ01358 standard; DNA; 19

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                                                                                                                                                                                                                                                          *tag= "these T residues are formed as part of a conventional phosphoramidite oligonuclectide synthesis process but using as the reactant a thymosine nucleoside having at the 3'-position a group of formula cH2-P(OGR2HZCN)-N(IPY)2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates, inter alia, to a method of preparing an oligonucleotide by coupling (1) a new nucleoside having a protected 5'-hydroxy group and at the 3'-position a group of formula -CH2-P(DR3)-NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy group, to give (3) a precursor having an internucleoside linkage of formula -CH2-P(DR3)-O-; and converting this to a linkage of formula -CH2-P(DR3) (=X)-O- (where X = S or O). The present sequence is a specific example of an oligonucleotide so
                                                Gaps
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                                                                                                                                                                               Oligonucleotide containing modified internucleotide linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetrahydrofuran derivatives - useful in the synthesis of
                            Length 19;
                         1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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         Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                Douglas ME,
                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; Page 29; 37pp; English.
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                                                              1084 AAAAAAAAAAAAA 1100
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                                                                               19 AAAAAAAAAAAAAA
                                                                                                                          AAV06820 standard; DNA; 19
                                                                                                                                                                (first entry)
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Best Local Similarity 100.1
Matches 17; Conservative
                                            17; Conservative
                                                                                                                                                                                                                                               16..18
/*tag=
                                                                                                                                                                                                   oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-052233/05.
                         Query Match
Best Local Similarity
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modified_base
                                                                                                                                                               13-OCT-1998
                                                                                                                                                                                                                                                                                                                     WO9747636-A2
                                                                                                                                                                                                                                                                                                                                                          03-JUN-1997;
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                                                                                                                                                                                                                    Synthetic.
                                                                                                                                            AAV06820;
                                                                                                        Matches
X S
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Use of a prostate cancer associated gene and biallelic markers

Claim 4; Page 374; 385pp; English.

Cohen D;

Chumakov I,

Bougueleret L,

Blumenfeld M, (GEST) GENSET

WPI; 1999-405178/34.

derived from it

98WO-IB02133 98US-0099658 97US-0996306

22-DEC-1998; 09-SEP-1998; 22-DEC-1997;

01-JUL-1999.

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The invention relates to a mammalian PG1 gene and protein, and a set of PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate specific Barly-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic
                                                                                                                                                                                                                                                                                                                     procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Indels

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19 ААААААААААААА 3

4AX81316/c

C6 derivative of (dT)"

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C6 derivative (dT)"

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quenched fluorescent moiety; biological assay; detection; identification; microorganism; sterilization assurance; nuclease; ss.
                                                                                                                                                                                                                                                                                                                            An enzyme-specific cleavable polynucleotide substrate bearing quenched fluorescent moieties
                                                                                                                                                                           //tag= d
/note= "amine-modified C6 derivative of
deoxythymidine (df)"
                                                                                                                                                     /note = "amine-modified C6 derivative of deoxythymidine (dr)"
                Enzyme-specific cleavable polynucleotide substrate;
Polynucleotide strand with amino groups.
                                                                                                             /*tag= b
/note= "amine-modified (
deoxythymidine
                                                                              /*tag= a
/note= "amine-modified /
deoxythymidine
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                           (MINN ) MINNESOTA MINING & MFG CO.
                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 20; 34pp; English
                                                                                                                                                                                                                                                                                                                                    fluorescent moieties
                                                                                                                                                                                                                                             98WO-US17311
                                                                                                                                                                                                                                                             98US-0005260
                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                           WPI; 1999-419356/35.
                                                                                                                                                                                                                                                                                            Wei A;
                                                                      modified base
                                                                                                                                                                     modified base
                                                                                                     modified_base
                                                                                                                                     modified base
                                                                                                                                                                                                             WO9935288-A1
                                                                                                                                                                                                                                            20-AUG-1998;
                                                                                                                                                                                                                                                            09-JAN-1998;
                                                                                                                                                                                                                            15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           levels of
                                               Synthetic
                       quenched
                                                                                                                                                                                                                                                                                           Mach PA,
                                                               Key
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The specification describes an enzyme-specific cleavable polymucleotide substrate bearing quenched fluorescent moieties. The enzyme-specific cleavable polymucleotide substrate is useful in biological assays for detection and identification of microorganisms, sterilization assurance, biological assays. The method provides a rapid and convenient approach for detection and identification of microorganisms. It can be adapted to sequence-dependent or sequence-independent tests. The invention provides improved accuracy, faster detection, and overall lower cost in detection and identification of microorganisms. The presence of nuclease is measured more accurately and sensitively by red-shifting the emission wavelength from far UV region (350-400 mm) to the 500-600 mm region of the electromagnetic spectrum and reducing the effect of background signal converse of the inventor sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
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1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                        Local Similarity
es 17; Conserv
                                        Query Match
                                                        Best Loca
Matches
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1084 AAAAAAAAAAAAA 1100
                       AAAAAAAAAAAAAA 3
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Conservative

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Gaps

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19 дададададададад 3

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Gaps · 0

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The specification describes a self-addressable, self-assembling microelectronic device which is designed to actively carry out and control multi-step and multiplex molecular biological reactions in microscopic formats. A key aspect of this inventions is played by the ion-permeable permeation layer which overlies the electrode. This permeation layer allows attachment of nucleic acids to permit immobilization but also separates the attached oligonucleotides and hybridized target DNA sequences from the highly reactive electrochemical environment generated immediately at the electrode surface. The microelectronic device is designed and fabricated to actively carry out and control reactions such as nucleic acid hybridizations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody/antigen reactions, sample preparation, diagnostics and biopolymer synthesis. The device can electronically control the transport and attachment of specific binding entities, such as nucleic acids and polypeptides, to specific micro-locations. The device can subsequently control the transport and reaction of analytes or reactants at the addressed specific micro-locations. The device is able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          concentrate analytes and reactants, remove non-specifically bound molecules, provide stringency control for DNA hybridization reactions
                                                                                                                                     Microelectronic device; multi-step reaction; microscopic format; ion-permeable permeation layer; electrode; electrical control; transport; attachment; binding; DNA/RNA hybrid; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sosnowski RG;
                                                                                                                                                                                                                                                                                  /*tag= a
/note= "amino group attached at 5' terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New microelectronic device designed to carry out and control multi-step and multiplex molecular biological reactions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 1; Lengtn 15; Pred, No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a probe used to exemplify the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edman CF, Heller MJ, Nerenberg MI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             improve the detection of analytes.
                                                                                                                                                                                                                                               Location/Qualifiers

 amino oligonucleotide probe T-2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.55,
100.0%; Pre-
AAX81316 standard; DNA; 19 BP
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                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-385567/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microscopic format
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1998;
                                                                     20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Butler WF,
                                                                                                                                                                                                            Synthetic
                                  AAX81316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for geometry allows the oligonucleotide acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
                                                                                                                                       Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             mod_base= OTHER
note= "3'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                    note= "3'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                             note= "3'-0-(2-methoxyethyl)thymidine"
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/mod_base= OTHER
/note= "3'-0-(2-methoxyethy1)thymidine"
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                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                           *tag= a
'mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                  base= OTHER
                        AAA88947 standard; DNA; 19 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0303586.
                                                                                                            Oligonucleotide ISIS 22110
                                                                               05-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohan V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672833/65.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-1999;
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                                                                                                                                                                                                 Synthetic
                                                   AAA88947;
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Gaps

0;

Query Match
1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

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New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNABSE-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'.-0'.(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form
                                                                                                                                                                                  Oligonuclectide, nuclease resistance, psoriasis, antipsoriatic, dermatological, cytostatic, virucide, antibacterial, fungicide, therapy, diagnosis, DNA-RNA hybrid, ss.
                                                                                                                                                                                                                                                                                                                           'note = "2'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "2'-0-(2-methoxyethy1)thymidine'
                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "2'-0-(2-methoxyethy1)thymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/mod_base= OTHER
/note= "2'-0-(2-methoxyethyl)uridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 54; Page 69; 132pp; English.
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /*tag= a
/mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/mod_base= OTHER
                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/label= RNA
19 AAAAAAAAAAAAAA
                                                                      AAA88948 standard; DNA; 19
                                                                                                                                                        Oligonucleotide ISIS 22111.
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                       *tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
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modified_base
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                                                                                                                              05-MAR-2001
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                                                                                                                                                                                                                                         Synthetic.
                                                                                                AAA88948;
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                                                         AAA88948/c
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Gaps

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affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide, nuclease resistance, psoriasis, antipsoriatic, dermatological, cytostatic, virucide, antibacterial, fungicide, therapy, diagnosis, DNA-RNA hybrid, ss.
to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonuclectides. Novel oligonuclectides of the invention have both A- and B-form
                                                                                                                                            "mod_base= OTHER
'note= "2'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mod_base= OTHER
note= "2'-0-(2-methoxyethy1)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "2'-0-(2-methoxyethyl)thymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "2'-O-(2-methoxyethy1)uridine"
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/*tag= f
/note= "phosphorothioate linkage"
                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                               100.0%; Preq. ...
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base= OTHER
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/label= RNA
                                                                                                                                                                                                      1084 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                      AAA88950 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide ISIS 22113
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                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mohan V;
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                                                                                                                                                                                                                                                                RESULT 289
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide ISIS 22112 contains a phosphorothicate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments
  inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications
                                                                                                                                                                                                                                                                                     Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.
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0
                                                             Length 19;
                                                                                   0; Indels
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/mod_base= OTHER
/note= "3'-0-(2-methoxyethy1)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                         note= "3'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= c
mod_base= OTHER
'note= "3'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        not\overline{e}= "3'-0-(2-methoxyethyl)thymidine'
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note= "phosphorothioate linkage"
                                                            Score 17; DB 1;
Pred. No. 2e+02;
                                      Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                     1.5%; Sc._
100.0%; Pred. No. _
'*** 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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'mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                            base= OTHER
                                                                                                           1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                           AAA88949 standard; DNA; 19 BP.
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                                                                                                                                  AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                Oligonucleotide ISIS 22112
                                                                                                                                                                                                                                         (first entry)
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                                                                                   17; Conservative
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC.
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                                                             Query Match
Best Local Similarity
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modified_base
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AAA88949/c
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Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has 2'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for Rhass-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications.
                                         New oligonucleotides containing sequences with A and B geometry, user to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/mod_base= OTHER
/note= "3'-0-(2-methoxyethy1)thymidine"
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/note= "3'-0-(2-methoxyethy1)thymidine"
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'note= "3'-O-(2-methoxyethy1)thymidine"
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/note= "phosphorothioate linkage"
                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                 Example 54; Page 69; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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'mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA88951 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide ISIS 22114
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Best Local Similarity 100.
Matches 17, Conservative
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             WPI; 2000-672833/65
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA88951;
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AAA88951/c
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Gaps

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Oligonuclectide ISIS 22114 contains a mixed phosphodiester and phosphorothicate backbone and has 3'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of cligonuclectides. Novel oligonuclectides of the invention have both A - and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonuclectide. The B-form geometry allows the oligonuclectide to serve as substrate for Rhase-H when bound to a target nucleic acid strand. The oligonuclectides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and
                                                                                                                                                                New oligonucleotides containing sequences with A and B geometry, user
to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
and bacterial infections, bind to single stranded RNA or DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                               fungal infections, and in various diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "2'-0-(2-methoxyethyl)thymidine"
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note= "2'-0-(2-methoxyethyl)thymidine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                              Example 54; Page 69; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/mod_base= OTHER
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 AAAAAAAAAAAAA 1100
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ID AAA88952 standard; DNA; 19 BP.
              03-MAY-2000; 2000WO-US11913.
                                             99US-0303586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide ISIS 22115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                     WPI; 2000-672833/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
modified_base
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                                         03-MAY-1999;
                                                                                                      Manoharan M,
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Matches
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oligonuclectides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonuclectide. The B-form geometry allows the oligonuclectide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The inflammatory skin conditions, skin cancers and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotides containing sequences with A and B geometry, user to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Il9 diester; nuclease stability assay; polymerase chain reaction; PCR; molecular cloning; disease diagnosis; disease treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents 2'-modified chimeric oligonucleotides containing 2'-modified T. The nucleotides were used to examine the effects of the modifications on nuclease resistance. Novel
    2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)"
                                                                                                                                       /*tag= c
/mod base= OTHER
/note= "2'-modified thymidine, i.e. -S-Me, -Me,
/note= "2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)'
                                      /*tag= b
/mod_base= OTHER
/mote= "2-modified thymidine, i.e. -S-Me, -Me
/note= "2-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)
                                                                                                                                                                                                                                                             /mcd_base= OTHER
/note= "2'-modified thymidine, i.e. -S-Me, -Me,
/sote= "2'-ara-(5), 2'-ara-(0Me)'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T19 diester for use in nuclease stability assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0303586.
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                                                                                                                                                                                                                                                /*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mohan V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-672833/65.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           WO200066609-A1.
                       modified base
                                                                                                                        modified base
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      D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide ISIS 22115 contains a mixed phosphodiester and phosphorothioate backbone and has 2'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of cligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the cligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.
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/mod_base= OTHER
/note= "2'-modified thymidine, i.e. -S-Me, -Me,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
note= "2'-0-(2-methoxyethyl)uridine"
                                 /*tag≈ e
/label= RNA
/label= RNA
/*tag= f
/*tag= f
/note= "phosphorothioate linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

    Modified chimeric oligonucleotide.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                              Mohan V;
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                                                                                                                                                        40200066609-A1
                                                                            modified base
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modified_base
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                misc_RNA
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09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2000,
                    nucleotide
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                               AAA71630;
                                                                                                                                                     Query Match
                                                                                                                                                                                                                              RESULT 295
AAA71630/c
                                                                                                                                                                     Matches
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                                                                                                                                                                                The present invention is concerned with methods of determining the nuclease stability of oligomeric compounds using capillary-gel electrophoresis and laser-induced fluorescence. The methods are useful in the polymerase chain reaction (PCR), molecular cloning and disease diagnosis and treatment. The present sequence was used in a demonstration
                                                                                                                                Determining the nuclease stability and relative binding affinity of an oligomeric compound comprises capillary gel electrophoresis using
                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage of nucleic acids from solid supports assay oligonucleotide #3
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detaching nucleic acid molecule comprising unconventional nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid cleavage, solid support, DNA-RNA hybrid, affinity chromatography, sequencing, mutagenesis, DNA preparation, nucleic acid purification; ss.
                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                           Score 17; DB 1; Length 19;
Pred. No. 2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                    Example 3; column 19-20; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                      1.5%; Scor
100.0%; Pre
0;
                                                                                                                                                                                                                           the methods of the invention.
                                                                                                                                                                                                                                                                                             1084 AAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                  99US-0234237
                                                                99US-0234237
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                                                                                                                                                  laser-induced Fluorescence
                                                                                                                                                                                                                                                                                                                                               .454/c
AAC62454 standard; DNA; 19
                                                                                                                                                                                                                                                                                                            19 AAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                 (ISIS-) ISIS PHARM INC.
                                                                                                  Cummins LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GOLD/) GOLDSBOROUGH
                                                                                                                  WPI; 2000-637737/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPI; 2000-664908/64
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200058329-A1
                                                  20-JAN-1999;
                                                                 20-JAN-1999;
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               US6127124-A
                                 03-OCT-2000
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Synthetic.
                                                                                                  Leeds JM,
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misc_RNA
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Best Local
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                                                                                                                                                                                                                      from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, cDNA and template preparation, DNA-based assays, mutagenesis procedures, mucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used in assays to demonstrate the methods of the invention.
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                                                                                                                                                                                              The present invention is concerned with the cleavage of nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel synthetic method (M) comprising: (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel method for the production of oligomers with reduced exocyclic adducts comprises treatment with deprotecting and cleaving reagents
incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 19; 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "phosphorothioate linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 17; DB 100.0%; Pred. No. 2e+cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorothioate 20-mer primer DNA #1.
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                                                                                                                                Example 3; Page 34; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
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WPI; 2000-205668/18.
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                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                               AAZ61390;
                                                                           Query Match
                                                                                                                                                                                 RESULT 297
                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to aminooxy-modified nucleosides and oligonuclectides and to oligonuclectides that elicit RNase H for cleavage in a complementary nuclect acid strand. It also relates to oligonuclectides wherein at least some of the nucleotides are oligonuclectides wherein at least some of the nucleotides are include a substituent that potentiates hybridisation of the nucleotides oligonuclectide to a complementary strand, and at least some of the nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The inclusion of one or more aminooxy moieties in such oligonuclectides provides for improved binding of such oligonuclectides to a complementary strand. The oligonuclectides of the invention are used as diagnostic, therapeutic or research reagents, and can be used to modulate gene expression in organisms. The oligonuclectides containing the modified nucleosides have increased nuclease resistance and increased binding
oligomers with a reduction in the number acrylonitrile groups attached. Acrylonitrile has been demonstrated to be a potent carcinogen in rats. This sequence represents a phosphorothioate 20-mer primer which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                           a
"These nucleotides are substituted with 2'-0-{2-
[N-(2-amino)ethyl-N-(methyl)]aminooxyethyl}
group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aminooxy-modified nucleosides and oligonucleotides useful in diagnostic, therapeutic and research reagents and for modulating the expression of protein in organisms -
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                           Modified nucleoside, aminooxy group,
2'-deoxy-erythro-pentofuranosyl sugar moiety, nuclease resistant,
hybridisation, binding affinity, ss.
                                                                                                            0;
                                                                                    Length 19;
                                                                                 1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Modified T-containing oligonucleotide, SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawasaki AM;
                                                           Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                 1084 AAAAAAAAAAAAAA 1100
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                                                                             Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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modified_base
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AAA06839/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents -
affinity to a complementary strand. The present sequence represents an oligonucleotide containing nucleotides substituted with a 2'-0-{2-[N-(2-amino)ethyl-N-(methyl)]aminooxyethyl} group.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                           ..
0
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                                                                                                                Score 17; DB 1; Length 15; Pred, No. 2e+02;
                                                                                               Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
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                                                                                                                                                         100.0%; Prec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uniform phosphodiester oligonucleotide.
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"2'-modified T"
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"2'-modified
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"2'-modified
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Les 17; Conservative
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Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110; research reagent; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel modified oligonucleotides, useful in antisense methodologies, diagnostics, therapeutics and as research reagents
                                                                                                                                                                                      *tag= a
'note= "Phosphorothioate internucleotide linkage"
                                                                                                                                                                                                                                                                               /note= "Optionally all 3'-O-(2-methoxyhexyl) or
2'-O-(2-methoxyethyl)"
                                                                                         Modified oligonucleotide #3 ISIS # 22110.
                                                                                                                                                                Socation/Qualifiers
                                                                                                                                                                                                                                                              /*tag= c.
/mod_base= OTHER
                            AAZ95240 standard, DNA; 19 BP.
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                                                                      (first entry)
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Best Local Similarity
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                                                                                                                                                                                                         misc feature
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                                                                     05-JUN-2000
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                                                                                                                                             Synthetic
                                                 AAZ95240;
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       RESULT 299
AAZ95240/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an oligomeric compound containing 2'-O-modified ribosyl nucleosides. The oligomeric compound contains phosphodiester linkages. The 2'-O-modified nucleosides include ring structures that position the sugar moiety of the nucleosides preferentially in 3' endo geometries. The modified oligomeric compounds have increased binding affinity and increased nuclease resistance. The oligomeric compounds can be used in diagnostic, therapeutic and research reagents.
                                                                                                                                                                                  2'-0-modified ribosyl oligonucleotide with phosphodiester linkages.
                                                                                                                                                                                                                                                                                                                       b
"2'.-O-[2-N,N-dimethylaminoethyl)oxyethyl-5-
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                                                                                                                                                                                                                                                                                         "nucleosides linked by phosphodiester
DB 1; Lexes
0. 2e+02;
0; Indels
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                                                                                                                                                                                                       Oligomeric compound; 2'.-O-modified ribosyl nucleoside; 3' endo geometry; nuclease resistance; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                            Mismatches
       Score 17;
Pred. No.
                                                                                                                                                                                                                                                          Location/Qualifiers
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1.5%; Scc.
100.0%; Pre
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100.0%; Prr
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  Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           modified_base
                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                      Synthetic.
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d "Optionally all phosphorothioate internucleotide linkages"

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                                                             course of
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                                                    This sequence represents a modified oligonucleotide used in the courtet invention. The invention relates to oligonucleotides comprising nucleotides covalently linked together by internucleotide linkages wat least 1 nucleotide is linked to adjacent nucleotide by a 2',5' internucleotide linkage and bears a 3'-substituent. The oligonucleotides can be used in gene therapy and are also useful in antisense methodologies, diagnostics, therappeutics and as research
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0
                                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 17; DB 1;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
Example 54; Page 59; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 AAAAAAAAAAAAA 1100
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ID AAZ95241 standard; DNA; 19 BP.
XX
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1084 AAAAAAAAAAAAA 1100

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19 ААААААААААААА 3

AAZ95241;

Synthetic

misc_RNA

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The present invention relates to a method for preparing phosphorothioate oligonucleotides having at least one nucleoside with a 2' modification. The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid group having at least one nequence with a 2' modification in an acetonitrile. The present sequence was used to illustrate the method of the present invention. The method is useful for synthesising sulphurised 2' substituted phosphorothioate oligonucleotides, which may be used in molecular biological research, in applications such as anti-viral therapy, and for determining the stereochemical pathways of certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy; gene therapy; primer; phosphorothicate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing sulfurized 2' substituted phosphorothioate oligonucleotides useful in biological research, comprises phosphicylating the 5'-hydroxyl of a nucleic acid having a nucleoside with a 2' andification -
                                               Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i DB 1; Leus-
io. 2e+02;
0; Indels
                                                                                                                                                                                                                         /*tag= b
/mod_base= "OTHER"
/note= "Modified with 2'-O-methoxyethyl"
                                                                                                                                                                                     /note= "All bases are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human type II RNase H substrate oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheruvallath ZS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 17;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymes which recognise nucleic acids.
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Column 7; 7pp; English.
                                                                                                                                                                      "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000; 2000US-0481486.
                                                                                                                                                                                                                                                                                                                                                                                                    97US-0950779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 AAAAAAAAAAAAAA
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                                                                                                                                                                        mod_base=
                                                                                                                                     1..19
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-407218/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserv
            Oligonucleotide #8.
                                                                                                                       Key
modified_base
                                                                                                                                                                                                         modified base
                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1997;
                                                                                                                                                                                                                                                                                               US6242591-B1
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                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 302
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a modified oligonucleotide used in the course of the invention. The invention relates to oligonucleotides comprising nucleotides covalently linked to pether by internucleotide linkages where at least 1 nucleotide is linked to adjacent nucleotide by a tleast 1 nucleotide linkage and bears a 3'-substituent. The oligonucleotides can be used in gene therapy and are also useful in antisense methodologies, diagnostics, therapeutics and as research
                                                                                                    Antisense oligonucleotide, phosphorothioate, gene therapy, ISIS # 22111, research reagent, therapeutic, ss.
                                                                                                                                                                                                                                                                               '*tag= d
'note= "Optionally all phosphorothioate internucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                     a11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel modified oligonucleotides, useful in antisense methodologies, diagnostics, therapeutics and as research reagents
                                                                                                                                                                                                                               a
"Phosphorothioate internucleotide linkage"
                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/mod_base= OTHER
/note= "Optionally all 3'-O-(2-methoxyhexyl) or
2'-O-(2-methoxyethyl)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
                                                                     Modified oligonucleotide #3 ISIS # 22111.
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 54; Page 59; 75pp; English
                                                                                                                                                                                                                                                                                                                 linkages"
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                                  (first entry)
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/*tag=
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200004189-A1
                                                                                                                                                                                                                                                                                                                                  modified base
                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-1999;
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                                  05-JUN-2000
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Gaps

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reagents

Query Match

AAH46460;

HXXXH

RESULT 301 AAH46460/c

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Synthetic
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                                     misc RNA
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                                                                                                                                                                                                                                                                      The present invention provides a number of DNA-RNA oligonucleotides which can act as substrates for human RNase HI (a type II RNase). The sequence consists of two portions, one of which is capable of supporting cleavage of a complementary target RNA and the other of which is incapable of supporting such cleavage. These can be used to enhance the effectiveness of antisense therapies. The present sequence is an RNase H substrate used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense therapy;
                                                                                                                                                                                                                       Chimeric oligonucleotides that can serve as substrates for human RNase
H1, useful for enhancing the effectiveness of antisense gene therapies
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             ò
                                        /mod_base= OTHER
/mod= "optionally phosphorothicate backbone"
(6.19
/ttag= b
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/note= "optionally phosphorothioate backbone"
16..19
                                                                                                                                                                                                                                                                                                                                                Score 17; DB 1; Length 15; Pred. No. 2e+02; 0; Indels
                                                                        /mod_base= OTHER
/note= "optionally 3'-0-(2-methoxyethyl)
2'-0-(2-methoxyethyl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; RNase H type II; RNase H1 cleavage substrate;
gene therapy; primer; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human type II RNase H substrate oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                          Manoharan M;
                 location/Qualifiers
                                                                                                                                                                                                                                                        Example 54; Page 88; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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100.0%; Pre
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/*tag= a
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                                *tag=
                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                        Lima WF,
                                                                                                                                                                                                        WPI; 2001-343164/36.
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Best Local Similarity
Matches 17; Conserv
                                                                                                        WO200123613-A1
               Key
modified_base
                                                       modified_base
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modified_base
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                                                                                                                                                       30-SEP-1999;
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                                                                                                                        05-APR-2001
                                                                                                                                                                                        ST,
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                        Crooke
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AAH25738/c
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The present invention provides a number of DNA-RNA oligonuclectides which can act as substrates for human RNase HI (a type II RNase). The sequence consists of two portions, one of which is capable of supporting cleavage of a complementary target RNA and the other of which is incapable of supporting such cleavage. These can be used to enhance the effectiveness of antisense therapies. The present sequence is an RNase H substrate used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric oligonucleotides that can serve as substrates for human RNase
H1, useful for enhancing the effectiveness of antisense gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                    or
/*tag= b
//mod_base= OTHBR
/note= "optionally 3'-O-(2-methoxyethyl)
2'-O-(2-methoxyethyl)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene expression; gene therapy; diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                         Manoharan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 54; Page 88; 178pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                              29-SEP-2000; 2000WO-US26729.
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                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cook PD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-343164/36
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                                                                                                                                                                 WO200123613-A1
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                                                                                                                                                                                                              05-APR-2001
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PAC83664/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating disease caused
or diagnosing and treating
                                                             The present invention relates to nucleotide oligomers comprising monomer units. Oligomers modulate gene expression when hybridized by single- or double-stranded nucleic acid. They are useful for gene therapy, diagnostic and investigative purposes.
                                                                                                                                                  Gaps
        Guanidinium functionalized oligomers prepared from corresponding monomer units, are hybridizable with a specific RNA or DNA sequence, useful for diagnostic and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to C3' methylene hydrogen phosphate oligomers. The oligomers may be used as research reagents, for treating disease caused by undesired production of proteins and for diagnosing and treating AIDS and atherosclerosis.
                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                     DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS; atherosclerosis; ss.
                                                                                                                           DB 1; Length 19;
2e+02;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 1; Length 19;
Pred. No. 2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;
                                                                                                          Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligomers for use as research reagent, foby undesired production of proteins, and for
                                                                                                                            1.5%; Score 17; DB 100.0%; Pred. No. 2ettive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Α'n
                                             Example 26; Page 54; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 46; Page 74; 110pp; English.
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100.0%; Pre
0;
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                                                                                                                                                                           AAF31564 standard; DNA; 19
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cook PD, Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-138117/14.
                                                                                                                                                                                                                                                                                    ISIS sequence 32327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                   WO200102419-A1
                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1999;
                                                                                                                                                                                                                                                                   09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                AAF31564;
                                                                                                                           Query Match
                                                                                                                                                                                                          Best Loca
Matches
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à g

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The present sequence is a modified oligonucleotide.

2. -O-acetamido-modified nucleosides were used to produce oligonucleotides
which have enhanced nuclease resistance and superior hybridisation
properties than prior art. The oligomeric compounds are useful for
identification or quantification of ribonucleic acid and deoxyribonucleic
contidentification or quantification of ribonucleic acid and deoxyribonucleic
contidentification or quantification of ribonucleic acid and deoxyribonucleic acid molecule. They have a modified nucleoside monomer
and are specifically hybridisable with a preselected nucleotide sequence
contidential molecule. The oligomers are further useful in a
case useful in abnormal cell proliferation and tumour formation and
are useful in abnormal cell proliferation and tumour formation and
modification of expression of protein kinase C and cell adhesion
concludes such as ICAM. They are useful in the modulation of proteins
concluded to multidrug resistance and viral genomic nucleic acids such as
HOV, herpes viruses, Epstein-Barr virus, cytomegalovirus, papillomavirus,
concluded the patities of the patitus of the patities of the patiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "2'-0-N-[2-(dimethylamino)ethylacetamido]5MeU"
                                                                                                                                                                                                                                                                                       2'-0-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance; tumour formation; cancer; protein kinase C expression; cell adhesion molecule expression; multidrug resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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1.5%; Score 17; DB 1; Length 19;
100 0%; Pred. No. 2e+02;
100 0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser AS, Prakash TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAA 1100
                                           BP.
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3664/c
AAC83664 standard; DNA; 19
                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-069824/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
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                                                                                                                                                                                                         02-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                      AAC83664;
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Gaps

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1084 ААААААААААААА 1100

Conservative

17;

Matches

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19 AAAAAAAAAAAAA 3

RESULT 307

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The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
       Dihydroxy sugar moiety, 2'-0-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Alkylating 2' position of 2',3'-dihydroxy sugar molety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide #3 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                Prakash TP;
                                                                                                                                               2'-dimethylaminooxyethoxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 1; Le
Pred. No. 2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                Manoharan M,
                                                                                                                                              /note= "5-methyl, 2'. (2'-DMAOE) residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 46; Column 31; 24pp; English
                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Scor.
100.0%; Pre
                                                                                                                   /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cooling and reacting with ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                    99US-0227782
                                                                                                                                                                                                                                                                                    99US-0227782
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                                                                                                                                                                                                                                                                                                                                               Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD42000 standard;
                                                                                   Key
modified_base
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modified_base
                                                                                                                                                                                                                                                                                                                  SISI (-SISI)
                                                                                                                                                                                                                                                                                  08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                Kawasaki AM,
                                                       Unidentified
                                                                                                                                                                                            US6403779-B1
                                                                                                                                                                                                                                                      38-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2002
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                                                                                                                                                                                                                        11-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel method of selective alkylation of 2. 3. dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive seter: The method is useful for the preparation of 2. O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                                                                            /mod_base= OTHER
/note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"
                                                                                                                                         Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide #2 used to illustrate the method of the invention.
                                                                                                             Oligonucleotide #1 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prakash TP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%; Score 17; DB 100.0%; Pred. No. 2e+tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 46; Column 31; 24pp; English.
                                                                                                                                                                                                                   Location/Qualifiers
15..18
cooling and reacting with ester
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Best Local Similarity 100. Matches 17; Conservative
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RESULT 308 AAD41999/ ID AAD4: AAD41999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                         Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note = "5-methyl, 2'-dimethylaminooxyethyl residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide #4 used to illustrate the method of the invention.
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                                                                                                                                                                                      Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
/mod_base= OTHER
/note= "2'-methoxyethoxy (MOE) residues"
                                                                                                                                                                                      Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                      Manoharan M,
                                                                                                                                                                                                                                                                                                               Example 46; Column 31; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                      cooling and reacting with ester -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 AAAAAAAAAAAAA 1100
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AAD42001 standard; DNA; 19
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/*tag= a
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                                                                                                                                                                                    Fraser AS,
                                                                                                                                                         PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                               WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
modified_base
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                                         US6403779-B1
                                                                                               08-JAN-1999;
                                                                                                                             08-JAN-1999;
                                                                                                                                                                                    Kawasaki AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-2002
                                                                      11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD42001;
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The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligomucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dibydroxy sugar moiety, 2'-0-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                               Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with seter -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide #5 used to illustrate the method of the invention.
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                                                          Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "5-methyl, 2'-methoxyethyl residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prakash
                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD,
                                                          Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cook
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                          Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manoharan M,
                                                                                                                                                                                         Example 46; Column 31; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
99US-0227782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD42002 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                         Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC.
                             (ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-546338/58.
                                                                                     WPI; 2002-546338/58
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modified_base
                                                       Kawasaki AM,
08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD42002;
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The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with mucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, disgnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -
                                                                                          Example 46; Column 33; 24pp; English.
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Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

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DB 1; Length 19;
2e+02;
hes 0; Indels
            100.0%; Pred. No. 2e+
  1.5%; Score 17;
                                            1084 AAAAAAAAAAAAA 1100
                                                                     AAAAAAAAAAAAA
                       17; Conservative
Query Match
Best Local Similarity
Matches 17; Consery
                                                                    19
                                            à
                                                                  g
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.. 0

Gaps

0;

RESULT 312 AAD42003/c

BP. AAD42003 standard; DNA; 19 (first entry) 04-NOV-2002 AAD42003;

Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss. Oligonucleotide #6 used to illustrate the method of the invention.

Location/Qualifiers ಹ 16..19 /*tag= Key modified_base

Unidentified

US6403779-B1

/note= "5-methyl, 2'-0-propyl residues"

/mod_base= OTHER

11-JUN-2002.

99US-0227782 99US-0227782 08-JAN-1999; 08-JAN-1999;

PHARM INC SISI (-SISI)

Prakash Cook PD, Manoharan M, Fraser AS, WPI; 2002-546338/58. Kawasaki AM,

used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester position of 2',3'-dihydroxy sugar moiety of Alkylating 2'

The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear registance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,

Example 46; Column 33; 24pp; English.

cooling and reacting with ester

Example 46; Column 33; 24pp; English.

The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic

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solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "5-methyl, 2'-dimethylaminooxyethyl residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide #7 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                 Length 19;
                                                                                                                                                                                                                                                                                        1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                               1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 17, Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3113
AAD42004/(XX XX AAD4; XX AAD4; XX DID AAD4; XX DID YX XX DID XX AAD4; XX AAA
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                                                                                                                                                                                                                                                                                        Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -
                                      Gaps
                                                                                                                                                                                                                                                            Oligonucleotide #8 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "5-methyl, 2'-methoxyethyl residues"
    1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manoharan M,
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                             1084 AAAAAAAAAAAAA 1100
                                                                                                                                                                        BP.
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ID AAD42005 standard; DNA; 19
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                                  Conservative
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-546338/58.
Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                     Key
modified_base
                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISI (-SISI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawasaki AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6403779-B1
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                                                                                                                                                                                                 AAD42005;
                                                                                                                                        RESULT 314
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Prakash TP;

Cook PD,

Manoharan M,

Fraser AS,

Kawasaki AM,

WPI; 2002-546338/58.

(ISIS-) ISIS PHARM INC.

99US-0227782. 99US-0227782.

08-JAN-1999; 08-JAN-1999;

US6403779-B1 11-JUN-2002.

/*tag= a /mod_base= OTHER /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"

hybridisation affinity;

Oligonucleotide #12 used to illustrate the method of the invention.

(first entry)

04-NOV-2002

AAD42009;

BP.

AAD42009 standard; DNA; 19

AAD42009/

Dibydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisatior nuclear resistance; alkylation; therapeutic; diagnostic; ss.

Location/Qualifiers

Key modified_base Unidentified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprofic solvent, cooling, treating with base, warming, cooling and reacting with ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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100.0%; Pred. No. 2-
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 46; Column 35; 24pp; English.
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Best Local Similarity 100.
Matches 17; Conservative
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AAD42010/c
ID AAD420
XX
AC AAD420
XX
DT 04-NOV
XX
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Gaps

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0; Indels

1084 AAAAAAAAAAAAA 1100

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19 AAAAAAAAAAAAA 3

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The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of 6 ligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.
                                                                                                             /mod_base= OTHER
/note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide #23 used to illustrate the method of the invention.
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/mod_base= OTHER
/note= "2'-0-methyleneiminooxyethyl thymidine"
                                                                                                                                                                                                                                                                                                                                                                         Manoharan M, Cook PD, Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 46; Column 37; 24pp; English.
                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         Kawasaki AM, Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-546338/58.
                                                Key
modified_base
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modified_base
          Unidentified
                                                                                                                                                                                                                                                      08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD42020/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with base, warming, colling and reacting with nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligomucleotide used to illustrate the method of the invention.
                                                                                                                                                                                             /mod_base= OTHER
/note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
18..19
                                     Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
Oligonucleotide #13 used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide #14 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            /*tag= b
/mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 46; Column 35; 24pp; English
                                                                                                                                          Location/Qualifiers
16..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cooling and reacting with ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AAAAAAAAAAAAAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0227782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0227782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD42011 standard; DNA; 19
                                                                                                                                                                                  *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                           modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawasaki AM,
                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                          38-JAN-1999;
                                                                                                                                                                                                                                                                                                                                            US6403779-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD42011;
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Matches

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AAD42011/ ID AAD4 AC AAD4 XX AAD4 XX O4-N XX DE Olig XX Diby XW Diby XX NUCl

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Gaps

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The invention relates to detecting mutations in the BRCA1 and hMLH1 gene comprising subjecting a set of amplification products to two-dimensional DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a specific mutation in either the BRCA1 or the hMLH1 gene.

Also included are test kits for enabling BRCA1 or hMLH1 gene testing comprising short PGR primers given in the specification, mixed in 20 mM of Tris-HG1, 50 mM kG1, 25 micro M of GNTP, and 5 % formande.

The method is useful for detecting mutations in the BRCA1 (breast and ovarian cancer susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA mismatch repair gene). The present sequence is a PCR primer specific to hMLH1 used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying and detecting nucleic acids, particularly DNA hybridization probes, involves employing chain extending enzymes (e.g. telomerase) to elongate probes to render them readily detectable
Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting amplification products to 2-dimensional gel electrophoresis to produce a characteristic spot pattern for a specific mutation in either the BRCA1 or the hMLH1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reaction; tailed primer; primer; probe; identification; on; linear amplification scheme; chain extending enzyme;
                                                                                                                                                                                                                                                                                                                                          Length 19;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                        Query Match 1.5%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/mod_base= OTHER
/note= "biotinylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                      Claim 6; Page 21; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         1080 TATTAAAAAAAAA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999; 99US-136545P.
25-MAY-2000; 2000US-0580358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001; 2001US-0917138
                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL51520 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streifel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361176/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TULL/) TULLIS R H. (STRE/) STREIFEL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002031776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 telomerase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tailing read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tullis RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL51520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL51520,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                        The present invention relates to a novel method of selective alkylation of 2.'3'-dihydroxy sugar molecties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive seter. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The presett sequence is a modified oligomucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                             Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1; breast and ovarian cancer susceptibility gene; TGDS; human; two-dimensional DNA electrophoresis; tumour suppressor gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                  Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                                  Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast cancer; ovarian cancer; tumour.
                                                                                                                                                                                                                                                                                            Example 46; Column 41; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 AAAAAAAAAAAAA 1100
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                                                      99US-0227782.
                                                                                    99US-0227782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2000; 2000WO-IB01607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK94423 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCSC-) ACAD APPLIED SCI
                                                                                                                                                  Fraser AS,
                                                                                                                    PHARM INC
                                                                                                                                                                                WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-471507/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200236819-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                  SISI (-SISI)
                                                                                                                                                  Kawasaki AM,
                                                      08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2002
                        11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vijg J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
ABK94423/
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Gaps

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Identifying and detecting nucleic acids, particularly DNA hybridization probes, involves employing chain extending enzymes (e.g. telomerase) to
                                                                                                                                                                                          Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
                                                                                                                                                                                                         Query Match 1.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2e+ Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                           example from the present invention.
      Example 1; Page 5; 10pp; English.
                                                                                                                                                                                                                                          1100
                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                         19 AAAAAAAAAAAAAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001; 2001US-0917138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1999; 99US-136545P.
25-MAY-2000; 2000US-0580358
                                                                                                                                                                                                                                          1084 AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                 ABL51521 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streifel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TULL) TULLIS R H.
(STRE/) STREIFEL J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361176/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002031776-A1.
                                                                                                                                                                                                                                                                                                                                                                                telomerase; ss.
                                                                                                                                                                                                                                                                                                                                 01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RH,
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                ABL51521;
                                                                                                                                                                                                                                                                                                                                                                                                                      misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rullis
                                                                                                                                                                                                                                                                                  RESULT 321
                                                                                                                                                                                                                                                                                          ABL51521
                                                                                                                                                                                                                                                                                                 g
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The present invention describes a method for detecting a nucleic acid probe, which comprises using chain extending enzymes to elongate probes. The method comprises (a) tracting the sample with a chain terminating reagent to prevent polynuclectide chain growth from the nucleic acid in the sample; (b) contacting the sample with the probe containing a termination of termina capable of elongation by a chain extending enzyme, where the probe hybridises to the nucleic acid in the sample; (c) contacting the sample with a chain extending enzyme and its substrates, which elongates the probe; and (d) detecting the elongated hybridised probe. Also described is a method comprising: (a) treating nucleic acid molecules or modified nucleic acid in a sample with a reagent or reagents that render the nucleic acid chains unextendable by a non-template-dependent enzyme; (c) hybridising the treated molecules with a nucleic acid probe that includes an extendable terminus, under conditions where hybrids form; and (c) treating any hybrids formed with a nucleic acid archain that the chain where hybrids form;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elongating enzyme and its substrates, where any hybridised probe is extended. The method is useful for identifying and detecting nucleic acids, particularly DNA hybridisation probes. The present sequence represents a talling reaction exemplary primer, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Length 17, 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
mod_base= "OTHER"
/note= "2'-methyl thioethyl thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note = "2'-methyl thioethyl thymidine"
elongate probes to render them readily detectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 18 A; 0 C; 0 G; 1 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0%; Pred. No. 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methyl thioethyl modified oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 base= "OTHER"
                                                    Example 1; Page 5; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAAA 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAAAAAAAAAAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2002 (first entry)
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modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA91949;
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                                                                    The present invention describes a method for detecting a nucleic acid probe, which comprises using chain extending enzymes to elongate probes. The method comprises: (a) treating the sample with a chain terminating reagent to prevent polynucleotide chain growth from the nucleic acid in the sample; (b) contacting the sample with the probe containing a terminating capable of elongation by a chain extending enzyme, where the probe hybridises to the nucleic acid in the sample; (c) contacting the sample with a chain extending enzyme and its substrates, which elongates the probe; and (d) detecting the elongated hybridised probe. Also described is a method comprising; (a) treating nucleic acid molecules or modified nucleic acid comprising; (a) treating nucleic acid molecules with a nucleic acid molecules or the nucleic acid chains unextendable by a non-template-dependent enzyme; (b) hybridising the treated molecules with a nucleic acid probe that includes an extendable terminus, under conditions where hybrids form; and (c) treating any hybrids formed with a non-template dependent chain catended. The method is useful for identifying and detecting nucleic acids, particularly DNA hybridisation probes. The present sequence acids, particularly DNA hybridisation probes. The present sequence represents a tailing reaction exemplary primer, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Gaps

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/note= "2'-methyl thioethyl thymidine"

"OTHER"

pase=

US6277982-B1 21-AUG-2001.

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/*tag=

modified base

note= "2'-methyl thioethyl thymidine"

us09904568-1.rng

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/*tag= c
/mod_base= "OTHER"
                        Cook PD,
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        99US-0378665
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Best Local Similarity 100.
Matches 17; Conservative
                         Manoharan M,
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                (ISIS-) ISIS PHARM INC
                                 WPI; 2002-235143/29.
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modified_base
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        20-AUG-1999;
                         Fraser AS,
                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                   ABA91950;
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modified base
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a chimeric oligonucleotide having some 2'-methyl thioethyl modifications. This was compared with coligonucleotides with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951) modifications for resistance to snake venom phosphodiesterase. The assay revealed the nuclease resistance of the modified oligomers. The invention provides methods for the alkylation of alcohols, amines, thiols and their derivatives by cyclic sulfate interndiates. In particular, methods for the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and their analogues with cyclic sulfates to form the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-sulfate sand their analogues. The methods are especially useful for the preparation of for are precursors for the preparation of oligomeric compounds useful are therapeutics, diagnostics and research reagents.
                                                                                                                                                                                                            miny action or alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                        Kawasaki AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note = "2'-methoxyethoxy thymidine"
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'note= "2'-methoxyethoxy thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
                                                                                                                                        Jung ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methoxyethoxy modified oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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99US-0378665.
  20-AUG-1999;
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The present sequence is that of a chimeric oligonucleotide having some 2'-methoxyethoxy modifications. This was compared with coligonucleotides with methyl thioethyl (see ABA9191949) and dimethylaminopropyl (see ABA91951) modifications for resistance to snake venom phosphodiseterase. The assay revealed the nuclease resistance of the modified oligomers. The invention provides ceristance of the modified oligomers. The invention provides contactives by cyclic sulfact intermediates. In particular, methods for the alkylation of the 2', 3' or 5'-hydroxy position of the 2', 3' or 5'-hydroxy position of corn the incleosides and their malogues with cyclic sulfates to form the Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile compounds are disclosed. Displacement of the 2', 3' or 5'-O-modified nucleosides and their analogues. The methods are especially useful for the preparation of the 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that are precursors for the preparation of oligomeric compounds useful
                                                                                                                                                                                                                                                                                                                                                                                 Alkylation of alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                          Kawasaki AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 17; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as therapeutics, diagnostics and research reagents
'note= "2'-methoxyethoxy thymidine"
                                                                            /note= "2'-methoxyethoxy thymidine"
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                                                                                                                                                                                                                                                                                                              Jung ME,
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16
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                                                          "OTHER"
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                                                          /mod_base=
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                                            *tag=
                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkylation of alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Kawasaki AM;
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                                                                                                                                  /*tag= c
/mod_base= "OTHER"
/note= "2'-dimethylaminopropyl thymidine"
                                  note= "2'-dimethylaminopropyl thymidine"
                                                                                                                                                                                                               /mod_base= "OTHER"
/note= "2'-dimethylaminopropyl thymidine"
                                                                                  /mod_base= "OTHER"
/note= "2'-dimethylaminopropyl thymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Jung ME,
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     /*tag= a
/mod_base= "OTHER"
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser AS, Manoharan M,
                                                                    /*tag=
                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                               PHARM INC
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(first entry)

16-APR-2002

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AAK98526,

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                                         Parget detection; quantitative analysis; probe; medical diagnosis;
forensics; bacterial screening; tissue typing; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schulz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining targets by interaction with probe array, useful e.g. fo
diagnosis, based on detecting formation of precipitate at specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclease resistant; ds; pharmaceutical; topical administration; transdermal patch; enzymatic degradation resistant.
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Nucleic acid quantitative analysis related oligonucleotide #1
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic nuclease-resistant oligomeric compound #54.
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                                                                                                                                                                                                                                     /*tag= a
/mod_base= OTHER
/note= "modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 47; 92pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001; 2001WO-EP07575.
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nes 17; Conserv
                                                                                                    genotyping; ss.
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                                                                                                                                                                                              Key
modified base
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                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002
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The invention relates to novel nuclease-resistant oligomeric compounds. The compounds of the invention are useful as pharmaceuticals for topica administration such as transdermal patches. The oligomeric compound is resistant to enzymatic degradation. The sequences shown in ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/mod_base= OTHER
/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"
                                                                                                                                       Nuclease-resistant oligomeric compound useful as pharmaceuticals topical administration such as transdermal patches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"
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/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide with 2'-0-(2-(methylthio)ethyl)-5-methyluridine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                1.5%; Score 17; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
100.0%; Pred. No. 100els
                                                                               Rajeev KG;
                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 25.1
Matches 17; Conservative 0; Mismatches
                                                                          Prakash TP,
                                                                                                                                                                                      Disclosure, Page 234; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AAAAAAAAAAAAA 2
          10-DEC-2001; 2001US-0013295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-2001; 2001US-302683P.
28-JAN-2002; 2002US-0058740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-2002; 2002WO-US20940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2003 (first entry)
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                                                                            Maier MA,
                                           (ISIS-) ISIS PHARM INC
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                                                                                                       WPI; 2003-247768/25.
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                                                                          Manoharan M,
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modified_base
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                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ58336;
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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel muclease-resistant oligomeric compounds. The compounds of the invention are useful as pharmaceuticals for topical administration such as transdermal patches. The oligomeric compound is resistant to enzymatic degradation. The sequences shown in ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                      Nuclease-resistant oligomeric compound useful as pharmaceuticals for topical administration such as transdermal patches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muclease resistant; ds; pharmaceutical; topical administration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic nuclease-resistant oligomeric compound #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transdermal patch; enzymatic degradation resistant
                                                                                                                                                                                                                                                                              Rajeev KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= "OTHER"
/note= "G-clamp modification"
                                                                                                                                                                                                                                                                      Manoharan M, Maier MA, Prakash TP,
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 234; 234pp; English.
                                               /note= "phenoxazine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                 base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1084 AAAAAAAAAAAAA 1100
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                                                                                                                                                                       03-JUL-2001; 2001US-302682P.
28-NOV-2001; 2001US-0996292.
10-DEC-2001; 2001US-0013295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AAAAAAAAAAAAA 2
                                                                                                                                            01-JUL-2002; 2002WO-US20934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2002; 2002WO-US20934.
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28-NOV-2001; 2001US-0996292.
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                  *tag= a
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                                                                                                                                                                                                                                           PHARM INC.
                                                                                                                                                                                                                                                                                                       WPI; 2003-247768/25
                                                                            WO2003004602-A2
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modified base
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modified_base
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                                                                                                            16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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Query Match

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ABZ75399;

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(GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ33554;
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 330
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                                                                                                                                                                                                                                The present sequence is an example of an oligonucleotide of the invention containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTB)-5-methyluridine) modifications. In examples of the invention, 2'-O-WTB was incorporated into oligonucleotides and evaluated for antisense properties in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOB) modification. The 2'-O-MTB modified oligonucleotides exhibited similar binding affinity to target RNA as their 2'-O-MOB equivalent while binding to human serum albumin was improved. The modification can be used to modulate the pharmacokinetics of oligonucleotides, e.g. in
                                                                                                                 Increasing binding of oligomeric compound to proteins useful in preparation of antisense therapeutics, involves use of modified oligomeric compound having oligonucleotide group
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Pred. No. 2e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dye-coupled 3'-amino modified oligonucleotide.
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100.0%; Pred. No. ...
... 0; Mismatches
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"3-amino modified"
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                                                                                                                                                                                                 Example 27; Page 72; 122pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AAAAAAAAAAAAA 1100
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(first entry)
                                       Prakash TP, Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
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/note=
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  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                              WPI; 2003-239204/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-201578/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA synthesis;
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02-DEC-1992
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XXX AAQ2

XXX AAQ2

XXX AAQ2

XXX DDT 02-D

DD 02-D

XXX DNA DNA XXX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                    nucleotide, it can be used in the synthesis of DNA and RNA nucleosides, nucleotides and oligonucleotides and for the synthesis of opposite strands in the presence of a template strand and in fluorescence microscopic and macroscopic detection in vivo and in vitro of genetic material. It is labelled with a fluorescent dye. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                     The sequence is an example of a dye coupled 3'-amino modified oligo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 1; Lo
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
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Example; Page 9; 17pp; German.
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(first entry)
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Matches 17; Conservative
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